10/009861 JC13 Rec'd PCT/PTO 10 DEC 2001

Application for United States Tetters Patent

To all whom it may concern:

Be it known that

Carlos Cordon-Cardo, Howard I. Scher, and Andrew Koff have invented certain new and useful improvements in

Markers For Prostate Cancer

of which the following is a full, clear and exact description.



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MARKERS FOR PROSTATE CANCER

This application claims priority of and is a continuation-inpart of U.S. Serial No. 09/329,917, filed June 10, 1999,
which is a continuation-in-part of PCT International
Application PCT/US98/25483, filed December 1, 1998, which
5 claims the benefit of U.S. Provisional Application No.
60/067,190, filed December 1, 1997, the content of which are
incorporated into this application by reference.

This invention was made in part with support under United 10 States Government NIH Grant CA-DK-47650. Accordingly, the United States Government has certain rights in the invention.

Throughout this application, various references are referred to within parentheses. Disclosures of these publications in their entireties are hereby incorporated by reference into this application to more fully describe the state of the art to which this invention pertains. Full bibliographic citation for these references may be found at the end the specification, preceding the claims.

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Background of the Invention

It has been postulated that the loss of function of a new family of negative cell cycle regulators, which act as cyclin-dependent kinase inhibitors and have been termed CKI, 25 might lead to tumor development. CKIs fall into two families, Kip and Ink, on the basis of sequence homology. implicated in G1 phase arrest by associating with multiple G1 cyclin-dependent kinases, abrogating their activity. However, no tumor-specific p27 genomic mutations have been 30 found in a large group of primary human cancers studied. More recently, it has been reported that proteasome-mediated degradation of p27 protein occurs during the cell cycle and that this degradation is increased in a subset of breast and Purpose: The present colon carcinomas of poor prognosis. 35 study was undertaken in order to assess for potential alterations of p27 expression in benign prostatic hyperplasia

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(BPH) and in a well characterized cohort of patients with prostatic cancer.

Inactivation of the p53 and RB tumor suppressor genes has 5 been implicated in the development and progression of a It has also been number of different cancers (1,2).postulated that the loss of function of a new family of negative cell cycle regulators, which act as cyclin-dependent kinase inhibitors and have been termed CKI, might also lead 10 to tumor development (3). CKIs fall into two families, Kip and Ink, on the basis of sequence homology (4). Kip family members include p21 (also known as WAF1, Cip1, or Sdil) (5-7), $p27^{Kip1}(8-10)$ and $p57^{Kip2}(11,12)$. The Ink group includes four members: p16^{INK4A/MTS1/CDKN2} (13), p15 ^{INK4B/MTS2} (14), 15 pl8 INK4C (15), and pl9 INK4D (16). p27 is a negative regulator implicated in G1 phase arrest by TGFS, cell-cell contact, agents that elevate cyclic AMP, and the growth inhibitory drug rapamycin (17-21). p27 associates with multiple G1 cyclin-dependent kinases in non-proliferating cells, 20 abrogating their activity (4, 8-10).

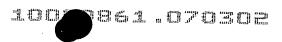
To assess its role as a potential tumor suppressor, the p27^{Kipl} gene was mapped to 12p12-12p13.1 and no tumor-specific genomic mutations in a large group of primary human cancers were observed (22-24). More recently, it has been reported that proteasome-mediated degradation of p27 occurs during the cell cycle and that this degradation is increased in a subset of breast and colon carcinomas of poor prognosis (25-28). The present study was undertaken in order to assess for potential alterations of p27 expression in BPH and in a well characterized cohort of patients with primary and metastatic prostatic cancer.

74 prostate carcinomas from primary and metastatic sites,
35 representing different hormone sensitivities were analyzed.
Normal prostatic tissues and cases of benign prostatic
hyperplasia were also studied. In order to evaluate
prostatic tissue of p27 null mice, eight 7 month old and six



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greater than 12 month old littermate pairs of wild-type and p27 knockout animals were used. Levels of expression and and RNA protein localization of p27 microanatomical transcripts were determined by immunohistochemistry and in 5 situ hybridization with specific antibodies and probes, analyses Comparative respectively. and immunodepletion immunohistochemistry, immunoblotting of also conducted in a subset assays were expression Association between alterations p27 in 10 clinicopathological variables were evaluated using Disease relapse-free two-tailed Fisher's exact test. survivals were evaluated using the Kaplan-Meier method and the Logrank test. Distinct anomalies in the expression of p27 in benign and malignant human prostate tissues are reported. 15 The normal human prostate shows abundant amounts of p27 and high levels of p27 messenger in both epithelial and stroma However, p27 protein and transcripts are almost undetectable in epithelial and stroma cells of BPH lesions. It is also reported that p27-null mice develop hypercellular 20 prostatic glands which histologically resemble human BPH. Based on these findings we postulate that the loss of p27 expression in human prostate may be causally linked to BPH. Prostatic carcinomas can be categorized into two groups: those that contain detectable p27 protein and those that do 25 not. In contrast to BPH, however, both groups of prostatic carcinomas contain abundant p27 transcripts. Moreover, primary prostatic carcinomas displaying the p27-negative phenotype appear to be biologically more aggressive, based on their association with time to prostate specific antigen 30 (PSA) failure following radical prostatectomy. These results support the postulate that BPH is not a premalignant lesion in the pathway of prostate cancer development. suggest that prostatic carcinoma develops along two different pathways, one involving the loss of p27 and the other using 35 other processes that circumvent the growth suppressive effects of p27.



Summary of the Invention

This invention provides a method for determining the aggressiveness of a prostate carcinoma comprising: (a) obtaining a sample of the prostate carcinoma; and (b) detecting the presence of p27 protein in the prostate carcinoma, the absence of p27 indicating that the prostate carcinoma is aggressive.

This invention also provides a method for diagnosing a beign prostate hyperplasia comprising: (a) obtaining an appropriate sample of the hyperplasia; and (b) detecting the presence of the p27 RNA, a decrease of the p27 RNA indicating that the hyperplasia is beign. In an embodiment, the above method further detects the protein expression of p27 wherein this additional step may be performed before or after the detection of the presence of the p27 RNA.

This invention provides a method for predicting the life-span of patient with prostate carcinoma comprising: (a) obtaining 20 a sample of the prostate carcinoma; and (b) detecting the presence of p27 protein in the prostate carcinoma, the presence of the p27 protein indicating that the patient can live longer than the patient who are undetectable p27 protein.

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This invention also provides a method for increasing the life-span of patient with prostate carcinoma comprising inducing the expression of p27 protein in the prostate carcinoma.

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This invention provides a method for prolong life-span of patient with prostate carcinoma which comprises introducing a nucleic acid molecule having sequence encoding a p27 protein into the carcinoma cell under conditions permitting expression of said gene so as to prolong the life-span of the patient with said prostate carcinoma. In an embodiment, the nucleic acid molecule comprises a vector. The vector includes, but is not limited to, an adenovirus vector, adeno-



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associated virus vector, Epstein-Barr virus vector, Herpes virus vector, attenuated HIV virus, retrovirus vector and vaccinia virus vector.

5 This invention provides a method for prolong life-span of patient with prostate carcinoma which comprises introducing an effective amount of p27 protein into the carcinoma cell so as to thereby prolong the life-span of the patient with said prostate carcinoma.

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This invention provides a method for prolong life-span of patient with prostate carcinoma which comprises introducing an effective amount of a substance capable of stabilizing the p27 protein into the carcinoma cell so as to thereby prolong the life-span of the patient with said prostate carcinoma.

This invention provides a composition for prolong life-span of patient with prostate carcinoma which comprises an effective amount of a nucleic acid molecule having sequence 20 encoding a p27 protein and a suitable carrier.

This invention provides a composition for prolong life-span of patient with prostate carcinoma which comprises an effective amount of the p27 protein and a suitable carrier.

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This invention provides a composition for prolong life-span of patient with prostate carcinoma which comprises an effective amount a substance capable of stabilizing the p27 protein and a suitable carrier.

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This invention provides a method of treating prostate cancer in a subject comprising administering to the subject a therapuetically effective amount of anti-Her-2/neu antibody to the subject.

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This invention also provides a method of diagnosing prostate cancer in a subject which comprises: a) measuring the amount of Her-2/neu expressed by a prostate sample from the subject;



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and b) comparing the amount of Her-2/neu expressed in step (a) with the amount of Her-2/neu expressed by a normal prostate, wherein a higher amount of Her-2/neu expressed in step (a) indicates prostate cancer.

This invention further provides a method of diagnosing prostate cancer in a subject which comprises: a) measuring the amount of Her-2/neu expressed by a prostate sample from the subject; and b) comparing the amount of Her-2/neu expressed in step (a) with the amount of Her-2/neu expressed by known cancer cell lines, wherein a higher amount of Her-2/neu expressed in step (a) than in the known cancer cell lines indicates prostate cancer.

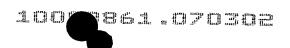
15 Brief Description of the Figures

Figures for the First Series of Experiments

Figure 1.

Histological analysis, immunohistochemistry, and in situ hybridization of human primary and metastatic prostatic 20 carcinomas.

- (A-C) Photomicrographs of primary prostatic carcinomas processed as follows: (A) Immunohistochemical staining against p27 of a prostatic intra-epithelial neoplastic (PIN) lesion; note the intense positive immunoreactivities observed in the nuclei of the tumor cells growing into the lumen. (B) Immunohistochemical staining against p27 of another PIN
 - Immunohistochemical staining against p27 of another PIN lesion showing dysplastic changes; note the intense positive immunostaining in the nuclei of normal epithelial cell and the low-to-undetectable staining of the tumor cells
- 30 dissecting the gland and growing into the lumen. ()
 Undetectable levels of p27 protein in an invasive primary
 prostatic carcinoma; note the staining of a normal gland
 trapped into the tumor.
- (D-F) Photomicrographs of metastatic prostatic carcinomas 35 processed as follows: (D) Immunohistochemical staining against p27 of a metastatic prostate carcinoma to lymph node; note the intense nuclear staining of both tumor cells and



lymphocytes (cells in the germinal center display low p27 levels). (E) Immunohistochemical staining against p27 of another metastatic prostate carcinoma to lymph node; note the intense positive immunostaining in the nuclei of lymphocytes and the undetectable levels of p27 staining on the tumor cells. (F) Immunohistochemical staining against p27 of a metastatic prostate carcinoma to bone; note the positive immunoreactivities in the nuclei of osteoblasts and the lack of staining of tumor cells.

10 (F and G) Photomicrographs of a primary invasive prostatic carcinoma processed as follows: (F) Low-to undetectable immunohistochemical staining against p27 in the tumor cells; note the staining of a normal gland trapped into the tumor. (G) In situ hybridization on a consecutive section from the case illustrated in panel (F) showing high mRNA levels of p27^{Kip1} even in p27-negative tumor cells utilizing the anti-sense probe to p27^{Kip1}. Original magnification (A) trough (F) 400x.

20 Figure 2.

In certain prostatic carcinomas p27 protein is a functional cyclin-dependent kinase inhibitor. (A) Immunohistochemical p27 with the presence correlates staining immunoblotting. Tumors #1 and #2 were negative and tumor #3 25 positive for p27 protein expression, paralleling their IHC patterns. (B) Immunodepletion of p27 extracts. Extracts obtained from tumors #2 and #3 were subjected to sequential depletion with antibodies specific to p27 or a non-specific rabbit anti-mouse (RaM). Following depletion, the proteins 30 in the supernatants were resolved and the presence of p27 determined by immunoblotting. (C) Depletion of p27 depletes heat stable cyclin-dependent kinase inhibitory activity. The boiled and following supernatant shown in panel B was clarification the soluble fraction was incubated with 35 different amounts of recombinant cyclin E/CDK2 kinase and the degree of inhibition of cylin E/CDK2 activity on histone H1 The amount of each kinase used is substrate was measured. shown in the panel and the bars are representative activities

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on an arbitrary scale. Depletion with either RaM or p27 specific antibodies did not affect the inhibitory activity of the p27 negative tumor; however, depletion of p27 from the positive tumor extract completely ablated the heat stable inhibitor activity.

Figure 3.

Recurrence-free proportion analysis of patients with primary prostate carcinoma (n=42) as assessed by time to detectable PSA. Patients who had PSA relapse were classified as failures, and patients with PSA relapse, or those who were still alive or died from other disease or lost to follow-up during the study period, were coded as censored. Time to relapse was defined as the time from date of surgery to the endpoint (relapse or censoring). Disease relapse-free survivals were evaluated using the Kaplan-Meier method and the Logrank test. A trend was observed between a p27 negative phenotype and early relapse (p=0.08).

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Figure 4.

Histological analysis, immunohistochemistry, and in situ hybridization of human normal prostate and benign prostatic hyperplasia.

- 25 (A-C) Photomicrographs of consecutive sections of normal prostate tissue processed as follows: (A) Immunohistochemical staining against p27; intense positive immunoreactivities are observed in the nuclei of epithelial cells in the luminal side of the acinus, with decreased reactivities in the nuclei of basal and stroma cells. (B) In situ hybridization showing high mRNA levels of p27^{Kip1} in both epithelial and stroma cells utilizing the anti-sense probe. (C) In situ hybridization utilizing the sense probe to p27^{Kip1} showing lack of signals in both epithelial and stroma cells.
 - (D-F) Photomicrographs of consecutive tissue sections of a benign prostatic hyperplastic nodule processed as follows:



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(D) Immunohistochemical staining against p27; note the lack or almost undetectable levels of immunoreactivity observed in the nuclei of both epithelial and stroma cells in the luminal side of the acinus, with decreased reactivities in 5 the nuclei of basal and stroma cells. (E) In situ hybridization showing low-to-undetectable p27 transcripts also in both epithelial and stroma cells utilizing the note the strong signal of the cellular anti-sense probe; inflammatory infiltrates that serve as an internal positive (F) In situ hybridization utilizing the sense probe to $p27^{\text{Kipl}}$ showing lack of signals in epithelial and stroma cells, as well as cellular inflammatory elements. Original magnifications: (A), (B) and (C) 1000x; (D), (E) and (F) 400x.

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Figure 5.

Histopathological analysis of the prostatic tissues of 12 month old p27+/+ (A) and p27-/- (B-D) mice. Photomicrographs of tissue sections of normal prostate samples processed as 20 follows: (A) Hematoxylin and eosin staining of a prostate gland of a p27+/+ mouse showing well defined acini of epithelial cells surrounded by a stroma containing few in supportive connective tissue fibroblasts and poor components. (B) Hematoxylin and eosin staining of a prostate 25 gland of a p27-/- mouse showing multiple and complex glands and hypercellular acini of epithelial cells surrounded by fibromuscular stroma cells in a connective tissue displaying abundant supportive components. (C and D) Hematoxylin and eosin stainings of a prostate gland of a p27-/- mouse, high 30 power details, illustrating the complexity of the glands and abundant fibromuscular stroma elements (C), as well as the hypercellularity of the acini (D). Original magnifications: (A) and (B) 200x; (C) and (D) 400x.

35 Figures for the Second Series of Experiments

Figure 6. Photomicrographs of selected primary prostate carcinoma cases analyzed by immunohistochemistry utilizing

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mouse monoclonal antibodies PAB1801 (anti-p53, A), 2A10 (anti-mdm2, B), Ab-1 (anti-p21, C), and MIBI (anti-Ki67, D). A, p53 nuclear overexpression in tumor cells. Note the positive nuclear staining of tumor cells at a perineural invasion site (arrow). B, mdm2 nuclear overexpression in tumor cells. C,p21 nuclear overexpression in tumor cells. D, high Ki67 proliferative index. Note the intense Ki67 nuclear staining of tumor cells at a perineural invasion site (arrow).

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Figure 7. Progression-free and survival curves for patients with primary prostate cancer. The Kaplan-Meier method was used to estimate overall disease free survival. The log-rank analysis was used to compare the different curves. A, progression was significantly reduced in patients with tumors displaying a p53-postive phenotype (P<0.01). B, progression was not related to mdm2 status. C, progression was significantly reduced in patients with tumors displaying a p21 positive phenotype (P=0.0165).

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Diagrammatic representation of the p53-pathway Figure 8. alterations that may develop during tumor and (A), progression in prostate cancer (B). (A) p53 regulates the expression of several genes involved in cell cycle arrest apoptosis and (ie, bax). p21 25 (ie, p21) heterodimeric protein kinases formed by cyclins cyclin-dependent kinases (Cdk's), blocking phosphorylation of pRB/E2F1 complexes and abrogating S-phase entry. p53 also produces an autoregulatory feed back loop by transactivating (B) Overexpression of mdm2 has been observed to occur 30 mdm2. in several tumor types, and it is considered an oncogenic binding to mdm2, p53 products Upon trasncriptionally inactivated and triggered for degradation. This will release the G1 arrest imposed, in part, by p21 and 35 abolish the apoptotic signals of the pathway. inactivation of p53 will favor proliferative activity,



immortality, and development/accumulation of further DNA damage or mutations. The increased p21 expression observed in our study could be produced via growth factor signaling, which would also impact on cyclin D1 expression. The increment of p21 does not appear to be able to control the proliferative activity of tumor cells, as attested by the association of p21 positive phenotype and high Ki67 proliferative index. Taken together, mdm2 overexpression will inactivate the p53-pathway, while increased mitogenic activity will offset the RB-pathway. The mechanistic basis for this dual requirement stems, in part, from the deactivation of a p53-dependent cell suicide program that would normally be brought about as a response to uncheked cellular proliferation resulting from RB-deficiency.

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Figures for the Third Series of Experiments

Figure 9A., Figure 9B., Figure 9C., Figure 9D., Figure 9E., and Figure 9F.

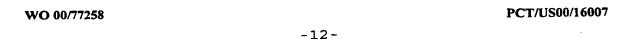
20 Figures for the Fourth Series of Experiments

Figure 10A-B. Immunohistochemistry and in situ hybridization of human benign prostatic hyperplasia (BPH). Consecutive sections of benign hyperplastic prostate tissue were processed as follows: A) Immunohistochemical staining of

25 pl6 is shown. Protein expression levels are undetectable in both epithelial and stromal components. B) In situ hybridization shows undetectable mRNA levels of pl6 in both epithelial and stromal components when the antisense probe is used.

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- Figure 11A-D. Immunohistochemistry and in situ hybridization of human primary prostatic carcinomas. Consecutive sections of primary human prostate cancer tissue were processed as follows: A) Immunohistochemical staining of p16 is shown.
- 35 Lack of immunoreaction noted in the nuclei and cytoplasm of both epithelial and stromal components. B) In situ



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hybridization reveals undetectable mRNA levels of p16 in both epithelial and stromal components when the antisense probe is used. (C-D) Histologic analysis, immunohistochemistry, and in situ hybridization of human primary prostatic carcinoma showing p16 overexpression. Consecutive sections of primary human prostate cancer tissue were processed as follows: C) Immunohistochemical staining of p16 is shown. Note strong brown immunoreaction observed in the nuclei of cells. Faint cytoplasmic staining is noted as well. D)

10 In situ hybridization shows high mRNA levels of p16 in epithelial cells when the antisense probe is used. A normal

epithelial cells when the antisense probe is used. A normal gland (see pointer) serves as an internal negative control in both the immunohistochemical analysis in Figure 11C and also the <u>in situ</u> hybridization analysis in Figure 11D.

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Figure 12. Kaplan-Meier curves, using the log rank test, stratified by p16 groups (group A or group B) of patients with primary prostate carcinoma (n=88) as assessed by time 20 to detectable PSA level post prostatectomy. Time to relapse was defined as the time from the date of surgery to the time of PSA elevation after surgery. The median time to relapse for group A has not been reached. The median time to relapse for group B was 46.25 months. Patients who had PSA relapse were classified as having treatment failures and tumor recurrence.

Figure for the Fifth Series of Experiments

Figure 13. Immunohistochemical staining of control cell
30 lines and primary prostatic carcinomas with anti-HER-2/neu
monoclonal antibody using the DAKO kit.

- A) Intense and homogeneous membrane staining in HER-2/neu overexpressing control cells (+3 category).
- B) Representative field of low to intermediate intensity 35 staining in <10% of control cells (÷1 category).
 - C) Representative area of HER-2/neu non-expressing control cells, showing negative immunohistochemical staining profile.



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D) Primary tumor displaying a strong membrane staining in tumor cells (÷2 category). Note the lack of immunoreactivities observed in the stroma elements.

- E) Primary tumor showing low expression levels of HER-5 2/neu; however, still membrane staining can be visualized (÷1 category).
 - F) Primary tumor with undetectable levels of HER-2/neu, representative of the negative phenotype cases. Original magnifications: A, B, C, and D and F, x400; E, x200.

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Detailed Description of the Invention

This invention provides a method for determining the aggressiveness of a prostate carcinoma comprising: (a) obtaining a sample of the prostate carcinoma; and (b) detecting the presence of p27 protein in the prostate carcinoma, the absence of p27 indicating that the prostate carcinoma is aggressive.

This invention also provides a method for diagnosing a beign prostate hyperplasia comprising: (a) obtaining an appropriate sample of the hyperplasia; and (b) detecting the presence of the p27 RNA, a decrease of the p27 RNA indicating that the hyperplasia is beign. In an embodiment, the above method further detects the protein expression of p27 wherein this additional step may be performed before or after the detection of the presence of the p27 RNA.

This invention provides a method for predicting the life-span of patient with prostate carcinoma comprising: (a) obtaining a sample of the prostate carcinoma; and (b) detecting the presence of p27 protein in the prostate carcinoma, the presence of the p27 protein indicating that the patient can live longer than the patient who are undetectable p27 protein.

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This invention also provides a method for increasing the life-span of patient with prostate carcinoma comprising inducing the expression of p27 protein in the prostate



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carcinoma.

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This invention provides a method for prolong life-span of patient with prostate carcinoma which comprises introducing 5 a nucleic acid molecule having sequence encoding a p27 protein into the carcinoma cell under conditions permitting expression of said gene so as to prolong the life-span of the patient with said prostate carcinoma. In an embodiment, the nucleic acid molecule comprises a vector. The vector 10 includes, but is not limited to, an adenovirus vector, adeno-associated virus vector, Epstein-Barr virus vector, Herpes virus vector, attenuated HIV virus, retrovirus vector and vaccinia virus vector.

- Methods to introduce a nucleic acid molecule into cells have been well known in the art. Naked nucleic acid molecule may be introduced into the cell by direct transformation. Alternatively, the nucleic acid molecule may be embedded in liposomes. Accordingly, this invention provides the above methods wherein the nucleic acid is introduced into the cells by naked DNA technology, adenovirus vector, adeno-associated virus vector, Epstein-Barr virus vector, Herpes virus vector, attenuated HIV vector, retroviral vectors, vaccinia virus vector, liposomes, antibody-coated liposomes, mechanical or electrical means. The above recited methods are merely served as examples for feasible means of introduction of the nucleic acid into cells. Other methods known may be also be used in this invention.
- 30 This invention provides a method for prolong life-span of patient with prostate carcinoma which comprises introducing an effective amount of p27 protein into the carcinoma cell so as to thereby prolong the life-span of the patient with said prostate carcinoma.

This invention provides a method for prolong life-span of patient with prostate carcinoma which comprises introducing an effective amount of a substance capable of stabilizing the



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p27 protein into the carcinoma cell so as to thereby prolong the life-span of the patient with said prostate carcinoma. Such substance may be either inhibiting the protease which degrade the p27 protein or it may interact with p27 in such a way that the protein will be resistant to degradation. By administering such substance into the cell, the effective amount of p27 protein will be increased.

This invention provides a composition for prolong life-span 10 of patient with prostate carcinoma which comprises an effective amount of a nucleic acid molecule having sequence encoding a p27 protein and a suitable carrier.

As used herein, the term "suitable carrier" encompasses any of the standard carriers. The composition may be constituted into any form suitable for the mode of administration selected. Compositions suitable for oral administration include solid forms, such as pills, capsules, granules, tablets, and powders, and liquid forms, such as solutions, syrups, elixirs, and suspensions. Forms useful for parenteral administration include sterile solutions, emulsions, and suspensions.

This invention provides a composition for prolong life-span 25 of patient with prostate carcinoma which comprises an effective amount of the p27 protein and a suitable carrier.

This invention provides a composition for prolong life-span of patient with prostate carcinoma which comprises an effective amount a substance capable of stabilizing the p27 protein and a suitable carrier.

This invention provides a method for determining the rate of proliferation of a prostate cancer comprising: (a) obtaining a sample of the prostate cancer; and (b) detecting the presence of p21 protein in the prostate cancer, the presence of p21 indicating that the prostate cancer will have a high proliferation rate.

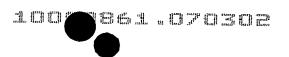
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This invention also provides a method for determining the rate of proliferation of a prostate cancer comprising: (a) obtaining a sample of the prostate cancer; and (b) detecting the mdm2 expression in the prostate cancer, the overexpression of mdm2 indicating that the prostate cancer will have high proliferation rate.

This invention provides a method for determining whether a prostate cancer would be metastatic comprising: (a) obtaining a sample of the prostate cancer; and (b) detecting the level of cyclin D1 expression in the prostate cancer, the overexpression of cyclin D1 indicating that the prostate cancer will be metastatic. In an embodiment, the prostate cancer is metastatic to bone.

This invention provides a method for determining the tumor recurrence in prostate cancer comprising: (a) obtaining a sample of the prostate cancer; and (b) detecting the expression of the cyclin-dependent kinase inhibitor pl6 in the prostate cancer, the overexpression of pl6 indicating that the prostate cancer will have high tumor recurrence.

This invention provides a method of treating prostate cancer in a subject comprising administering to the subject a 25 therapuetically effective amount of anti-Her-2/neu antibody to the subject. In an embodiment of the method, the prostate cancer is androgen-dependent. In another embodiment, the method of treating prostate cancer in a subject further administering to the subject an antitumor comprises 30 chemotherapeutic agent. In a still further embodiment of the method, the antitumor chemotherapeutic agent is selected from the group consisting of paclitaxel, doxorubicin, cis-platin, cyclophosphamide, etoposide, vinorelbine, vinblastin, 2-methoxyestradiol. In colchinin, and tamoxifen, 35 embodiment of the method, the prostate cancer is androgendependent. In another embodiment of the method, the prostate cancer is androgen-independent.



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This invention also provides a method of diagnosing prostate cancer in a subject which comprises: a) measuring the amount of Her-2/neu expressed by a prostate sample from the subject; and b) comparing the amount of Her-2/neu expressed in step 5 (a) with the amount of Her-2/neu expressed by a normal prostate, wherein a higher amount of Her-2/neu expressed in step (a) indicates prostate cancer. Standard amounts of Her-2/neu expressed by a normal prostate (or cell lines) to which to compare the amount of Her-2/neu expressed by a prostate 10 sample are available to one of skill.

This invention further provides a method of diagnosing prostate cancer in a subject which comprises: a) measuring the amount of Her-2/neu expressed by a prostate sample from 15 the subject; and b) comparing the amount of Her-2/neu expressed in step (a) with the amount of Her-2/neu expressed by known cancer cell lines, wherein a higher amount of Her-2/neu expressed in step (a) than in the known cancer cell lines indicates prostate cancer. Standard amounts of Her-2/neu expressed by cancer cell lines to which to compare the amount of Her-2/neu expressed by a prostate sample are available to one of skill.

This invention will be better understood from the 25 Experimental Details which follow. However, one skilled in the art will readily appreciate that the specific methods and results discussed are merely illustrative of the invention as described more fully in the claims which follow thereafter.

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EXPERIMENTAL DETAILS

Experimental Details for First Series of Experiments MATERIALS AND METHODS

Patient Characteristics and Tissues. A cohort of 74 patients
35 with prostatic carcinoma were evaluated. Tissues were
obtained from the Department of Pathology, Memorial
Sloan-Kettering Cancer Center, New York. Samples were

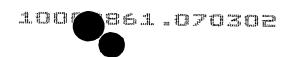
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formalin-fixed, paraffin-embedded tissue specimens. Fourty-two primary prostate adenocarcinoma specimens were evaluated, as well as 9 metastases to lymph node and 23 metastases to bone. Normal prostatic tissue and/or areas of 5 benign prostatic hyperplasia adjacent to tumor were observed in the majority of the primary cases studied. These tissues were also analyzed as part of the study. In addition, 10 pairs of frozen normal and tumor prostate tissues were utilized for antibody titration, as well as comparative 10 analyses between immunohistochemistry, immunoblotting and immunodepletion assays (see below). Representative hematoxylin-eosin stained sections were examined to evaluate the histopathological characteristics of the lesions to be analyzed, including the ratio of normal-to-tumor content for 15 microdissection techniques.

In order to evaluate prostatic tissue of p27 null mice, eight 7 month old and six greater than 12 month old littermate pairs of wild-type and p27 knockout animals were used. 20 Tissues were dissected, weighted and processed for histology by formalin fixation and paraffin embedding. Tissue sections were cutted and stained with hematoxylin-eosin for histologic analysis. All sections were utilized to count the number of acini per gland, a process that was conducted utilizing 25 magnifications of 200x.

Antibodies and Immunohistochemistry. The following well characterized antibodies and corresponding final working dilutions were used for the present study: monoclonal antibody p27/Kipl (Ab-2, Oncogene Science, Boston, MA - 0.1 ug/ml final concentration) and anti-p27 affinity purified rabbit antiserum (1:500 dilution). A non-immune rabbit serum and mouse monoclonal antibody MIgS-KpI were used as negative controls at similar working dilutions. Deparaffinized sections were treated with 3% H₂O₂ in order to block endogenous peroxidase activity. Sections were subsequently immersed in boiling 0.01% citric acid (pH 6.0) in a microwave oven for 15 minutes to enhance antigen retrieval, allowed to





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cool, and incubated with 10% normal horse or normal goat sera to block non-specific tissue immunoreactivities. Primary 4°C. were then incubated overnight at antibodies anti-mouse IgG antibodies (Vector horse Biotinylated 5 Laboratories, Burlingame, CA - 1:500 dilution) or goat anti-rabbit antibodies (Vector Laboratories - 1:800 dilution) were applied for lhour, followed by avidin-biotin peroxidase complexes for 30 minutes (Vector Laboratories -Diaminobenzidine was used as the final chromogen dilution). 10 and hematoxylin was used as the nuclear counterstain. Nuclear immunoreactivities were classified as a continuum data (undetectable levels or 0% to homogeneous staining or 100%). Tumors were grouped into two categories defined as follows: negative (0% or undetectable staining to <20% nuclear 15 immunoreactivity in tumor cells), and positive (neoplasms with >20% tumor cells with nuclear staining) (see statistical section).

Probes and In Situ Hybridization. Digoxigenin-labeled probes 20 were used for in situ hybridization and 1 ug of recombinant plasmid pCR™II (Invitrogen, San Diego, CA), containing the full length human p27 gene (gift of Dr. M. Pagano, New York University School of Medicine, NY) was linearized by BamHI and XbaI to generate antisense and sense transcripts. 25 Riboprobes were generated with T7 and SP6 polymerase for 2 1X transcription buffer (Boehringer at 37°C in Mannheim, Indianapolis, IN), 20 U of RNAse inhibitor, 1 mmol/L each of ATP, GTP, CTP, 6.5 mmol/L UTP and 3.35 mmol/L digoxigenin-UTP. Deparaffinized tissue sections were rinsed 30 in water and PBS for 10 minutes. The slides were digested with Proteinase K (50ug/ml) for 18 minutes at 37°C in PBS, and post-fixed at 4 °C in a freshly prepared solution of 4% paraformaldehyde in PBS for 5 minutes. Prehybridization was done for 30 minutes at 45 °C in 50% formamide and 2XSSC. 35 hybridization buffer consisted of 50% deionized formamide (v/v), 10% dextran sulphate (50% stock solution), 2XSSC (20X stock solution), 1% SDS (10% stock solution), and 0.25 mg/ml of herring sperm DNA (10 mg/ml). Hybridization was peformed

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overnight at 45 °C applying 10 pmol/L digoxigenin-labeled riboprobe in 50 ul of hybridization buffer per section under a coverslip. The coverslips were removed and the slides were washed in pre-warmed 2XSSC for 20 minutes at 60 °C twice, 5 followed by washes in pre-warmed 0.5XSSC and 0.01XSSC at 60 °C for 20 minutes, respectively. After these washes the slides were incubated in normal sheep serum diluted in buffer pH 7.5 and successively in the same buffer with antibody anti-digoxigenin-AP (Boehringer Mannheim, Indianapolis, IN) 10 at dilution of 1:1500 for 1 hour at room temperature. The visualization was accomplished by nitro-blue tetrazolium 5-bromo-4-chloro-3-indoylphosphate. slides The counterstained with methyl green and mounted.

15 Immunoblotting and Immunodepletion Assays. Proteins were extracted from three OCT-embedded prostatic carcinomas and resolved on polyacrylamide gels for immunoblotting with p27-specific antibodies. Extracts obtained from p27 positive and negative tumors were subjected to sequential depletion 20 with antibodies specific to p27 or a non-specific rabbit anti-mouse (RaM). Following depletion, the proteins in the supernatants were resolved and the presence of p27 determined Aliquots of these supernatants were by immunoblotting. briefly boiled and following clarification the soluble 25 fraction was incubated with different amounts of recombinant cyclin E/CDK2 kinase and the degree of inhibition of cylin E/CDK2 activity on histone H1 substrate was measured.

Statistical Methods. The statistical analyses were conducted 30 as follows. For alterations of the p27, we divided patients into two groups: p27 negative (0% or no immunohistochemical staining to <20% tumor cells displaying nuclear reactivities) or p27 positive (≥20% tumor cells with nuclear immunostaining The data analyses were conducted to explore the with IHC). 35 relationship between p27 alterations and clinicopathological presentation (primary, lymph as such variables metastases, and bone metastases), clinical stage (B, C, D), total Gleason score (6 or less versus 7 or more), and



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hormonal status (naïve versus androgen-independent) in a total 74 patients. For 42 patients with primary prostate cancer who underwent radical prostatectomy, further analysis was conducted to evaluate the relationship between p27 5 alterations and clinical variables, including those described above and PSA relapse (yes and no). Two-tail Fisher's exact test was utilized to assess these associations and two tailed p-values were employed as a significant level (29). procedure in SAS was used in this study (30). 10 analysis of disease relapse-free survival, patients who had PSA relapse were classified as lost failures, and patients with PSA relapse, or those who were still alive or died from other disease or to follow-up during the study period, were Disease relapse-free survivals were coded as censored. 15 evaluated using the Kaplan-Meier method (31) and the Logrank test (32). The LIFETEST procedure in SAS was used (30). Proportional hazards analysis was used to obtain maximum likelihood estimates of relative risks and their 95% confidence intervals (33,34).

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EXPERIMENTAL RESULTS AND DISCUSSION

Experimental Results and Discussion for the First Series of Experiments

To determine whether loss of p27 expression was a common 25 feature in prostate cancer, we analyzed 74 carcinomas from primary and metastatic sites, representing Included hormone sensitivities. different hormone-naïve primary tumors, some with associated prostatic intraepithelial neoplastic (PIN) lesions, and 32 metastatic 30 carcinomas from lymph node tumors (n=9) and bone metastases Thirteen of these metastatic lesions were from (n=23). hormone-naïve cases, while the remaining 19 metastases were obtained after hormonal treatment. PIN lesions displaying a cribiform or pseudopapillary pattern expressed high levels 35 of p27 protein (Figure 1A) and were associated with p27-positive invasive prostatic carcinomas. In contrast, PIN lesions displaying a flat growth pattern had low to undetectable p27 levels (Figure 1B) and were associated with

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p27-negative invasive tumors. Of the invasive primary prostatic carcinomas studied, 12 of 42 (28.5%) cases had an intense nuclear immunoreactive p27 pattern in the malignant cells (data not shown). The remaining 30 (71.5%) primary 5 neoplasms displayed altered patterns of expression: 12 cases had undetectable p27 levels (Figure 1C), while 18 cases had a heterogeneous pattern of expression (data not shown). metastatic lesions, 7 of 32 (21.9%) showed intense p27 nuclear immunostaining in most tumor cells (Figure 1D). The metastatic lesions had either (78.1%) 10 remaining 25 heterogeneous (data not shown) or undetectable nuclear expression of p27 (Figures 1E and 1F). Interestingly, all but one of the nine patients with hormone-independent bone lesions displayed altered p27 expression. Four of these 9 15 cases had undetectable p27 protein expression (Figure 1F), 4 cases had heterogeneous patterns of p27 expression ranging from 30% to 40% tumor cells with weak positive staining, and one case displayed 80% positive tumor cells. However, high determined by p27^{Kip1} mRNA, levels of as 20 hybridization to a p27 cDNA probe, were found in all tumors even when the lesions displayed undetectable levels of p27 protein (Figures 1G and 1H).

In the group of tumors that expressed p27, we next determined 25 if the p27 protein was inactivated. To accomplish this we extracted protein from fresh frozen samples and measured the heat stable Cdk inhibitory activity, using cyclin E/CDK2 as a substrate, remaining in extracts following depletion with p27-specific antibodies as described previously (17) (Figure confirmed p27 protein was Depletion of 30 2). immunoblotting. As expected, the depletion of extracts derived from p27 negative tumors did not affect the heat stable inhibitory activity, nor did depletion of p27 positive non-specific rabbit-anti-mouse extract with a 35 immunoglobulin. However, depletion of extracts derived from p27 positive tumors with the p27-specific antibody completely removed the inhibitory activity, indicating that p27 was functional as a Cdk inhibitor in these samples.



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Taken together, these data suggest that prostatic carcinomas develop along two different pathways, one involving the loss of p27 and the other using alternative processes that may circumvent the growth suppressive effects of p27. 5 to determine if these distinct pathways of prostate tumorigenesis correlate with clinical parameters, as reported for other tumor types (25-28), associations between p27 immunostaining, stage, total Gleason score, and hormonal status of the tumor were assessed. No associations between 10 detectable versus undetectable p27 protein, Gleason score (6 or less versus 7 or more), or hormonal status (naïve versus androgen-independent) were observed. To assess disease aggressiveness, we evaluated the time to PSA failure, the most sensitive indicator of success or failure following 15 radical prostatectomy, in patients treated for localized disease. Only patients who had an undetectable PSA level after surgery, an indication that the resection was complete, were considered. A trend toward an association was observed between a p27 negative phenotype and early relapse (p=0.08) This difference did not reach statistical 20 (Figure 3). significance due to the limited sample size of the cohort Supporting this concept is the fact that multivariate proportional hazards analysis, after controlling for stage and Gleason score, p27 status still was the 25 strongest factor in predicting PSA relapse (p=0.07).

These data suggest extending the characterization of p27 and benign prostatic prostate expression to normal hyperplasia. In the normal human prostate, abundant amounts 30 of p27 protein were detected in the ductal and acinar cells, mainly luminal elements, as well as stroma cells using immunohistochemistry. Epithelial cells displayed a strong nuclear immunostaining signal (Figure 4A). Likewise, both stroma cells expressed abundant epithelial and 35 transcripts (Figures 4B and 4C), as detected by in situ hybridization. Strikingly, in 12 cases of BPH p27 expression was low to undetectable in epithelial and stroma cells in the hyperplastic nodules. Immunohistochemical staining revealed



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low to undetectable immunoreactivities in both epithelial and fibromuscular cells in the hyperplastic nodules (Figure 4D). This contrasts with the strong p27 nuclear immunostaining phenotype observed in the normal prostate. Likewise, levels were low to undetectable 5 mRNA transcript consecutive sections of BPH by in situ hybridization (Figure 4E and 4F). In some of these BPH tissue samples we found areas of basal cell hyperplasia. These cellular elements also low to undetectable amounts of p27 protein (data not shown). Nevertheless, the 10 transcripts non-hyperplastic regions of these same BPH samples, normal ductal and acinar epithelial cells, as well as stroma elements, showed high levels of p27 expression. results indicate that in the development of BPH, 15 transcription may be down-regulated. This finding was quite unexpected as this gene product is generally regulated at post-transcriptional levels (35-37), although members of the nuclear hormone receptor superfamily are suggested to regulate p27Kipl mRNA levels (38).

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The targeted deletion of the p27 locus in a murine model was recently reported (39-41). p27 deficient mice are viable and display organomegaly, increased body size and These anomalies could not be attributed to a infertility. 25 defect of the growth hormone/IGF-1 axis, rather, they resulted from excess proliferation prior to withdrawal of cells into a terminally differentiated state (39). increased incidence of spontaneous tumors was observed; however, many p27-null mice developed a pituitary hyperplasia 30 reminiscent of adenoma in the intermediate lobe. These data suggest that p27 deficiency leads to hyperplasia in many The high frequency of benign prostatic tissues and organs. in men and the alterations on p27 (BPH) hyperplasia expression in that condition suggested a parallel to p27 35 deficiency. Previous reports of histopathological analyses of p27 null mice did not include the prostate (39-41). We next set up to determine the morphologic characteristics of the prostate gland in p27 deficient animals. Comparing the



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total mean prostate weights of 7 month old age-matched p27+/+ (n=8) and p27-/- (n=8) mice, the differences were not significant [mean +/- SD: 80.6 mg (+/- 8.6 mg) and 90.1 mg (+/-13.3 mg), respectively (p=0.1)]. However, the mean 5 acini counts of the total gland in these groups were significantly different [mean +/- SD: 50.4 (+/- 8.5) and (+/-8.9), respectively (p<0.01)]. Α relationship was observed in the mean total prostate weights of the old (greater than 12 months) p27+/+ (n=6) and p27-/-10 (n=6) mice [mean +/- SD: 114.0 mg (+/- 18.5 mg) and 119.0 mg (+/- 26.8 mg), respectively (p=0.7)], and the mean acini 54.7 (+/- 6.5) and 73.8 (+/- 5.3), counts [mean +/- SD: respectively (p<0.01)]. The significant increase in the number of acini in both young and old p27 deficient mice was 15 associated with histopathological differences that became more accentuated in the elderly group. The hyperplastic prostate of the older p27-/- mice showed enlarged glands, development of hypercellular acini of epithelial cells, and an increase in fibromuscular stroma cells (Figure 5). These 20 histological changes are reminiscent of BPH in humans and support the hypothesis that the loss of p27 expression in human prostate may be causally linked to BPH.

It has been suggested that BPH and malignant prostate growth 25 share a common pathway because they commonly coexist and demonstrate androgen dependency (42-44). However, this relationship remains unclear since BPH tends to develop in the transition zone, while the majority of carcinomas develop in the peripheral zone (45-48). Results from the present 30 study reveal that, unlike in the BPH lesions, prostatic expression the p27 cells regulate carcinoma Taken together these post-transcriptional level. support the postulate that BPH is not a premalignant lesion prostate cancer development.

Coordinate inactivation of the pathways involving the p53 and RB genes appears to be an essential requirement for the genesis of most human cancers. However, both p53 mutations

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and RB alterations are reported to be late and uncommon events in prostate tumor progression (49-52). Contrary to these results, data from this study indicate that inactivation of p27 is a frequent and early event in some prostate cancers. It is thus our working hypothesis that p27 represents another pathway of tumor suppression in certain human tumors, prostate cancer being a paradigm in which this concept could be further tested.

10 In summary, data from this study suggest that p27 kipl gene ablation in the mouse causes a pronounced prostatic hyperplasia, and that the loss of p27 expression in human prostate may be causally linked to BPH. In addition, data from this study suggest that prostatic carcinoma develops 15 along two different pathways, one involving the loss of p27 and the other using alternative processes that circumvent the growth suppressive effects of p27. These phenotypes can be identified as early as in the PIN stage. Moreover, primary prostatic carcinomas displaying the p27-negative phenotype 20 appear to be biologically more aggressive, based on their association with time to PSA failure following radical prostatectomy while controlling for other variables. consistent alteration of p27 expression observed in all lesions suggests androgen-independent metastatic 25 association with tumor progression, which may be the result of the metastatic process itself. Alternatively, it may be postulated that p27 positive tumors are more sensitive to androgen ablation, the primary treatment of metastatic Finally, two dissimilar mechanisms appear to be disease. 30 involved in the loss of p27 expression in BPH versus a subset of prostatic carcinomas. p27Kipl mRNA levels are extensively reduced in BPH, whereas p27 proteins are diminished to undetectable levels in some prostatic carcinomas despite detectable p27 mRNA as the result of a post-transcriptional 35 event. These results support the postulate that BPH is not a premalignant lesion in the pathway of prostate cancer development.

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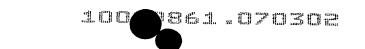
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SECOND SERIES OF EXPERIMENTS

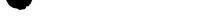
To determine the potential role of p53 inactivation in prostate cancer, we studied a well characterized cohort of 5 86 patients treated with radical prostatectomy. We analyzed mdm2, of p53, and p21/WAF1 expression immunohistochemistry. Results were then correlated with clinicopathological parameters of poor outcome, including time to PSA relapse. In addition, data were also correlated 10 with proliferative index, as assessed by Ki67 antigen detection. p53 positive phenotype, defined as identification of nuclear immunoreactivity in >20% tumor cells, was observed in 6 of 86 cases (7%). An association was observed between p53 positive phenotype and decreased time to PSA relapse 15 (P<0.01). mdm2 positive phenotype, defined as ≥20% tumor cells displaying nuclear immunoreactivity, was observed in 28 of 86 cases (32.5%). mdm2 positive phenotype was found to be associated with advanced stage (P=0.009). p21 positive phenotype, defined as >5% tumor cells with 20 immunoreactivity, was observed in 28 of 86 cases (32.5%). An association was observed between p21 positive phenotype and high Ki67 proliferative index (P=0.002). Patients with p21 positive phenotype had a significant association with decreased time to PSA relapse (P=0.0165). In addition, a 25 significant association was found between p21 positive phenotype and co-expression of mdm2 (P<0.01). Fourty-three of 86 cases (50%) were found to have one or more alterations, and patients with any alteration were found to have a higher rate of PSA relapse (P<0.01). It is our hypothesis that a prostate cancer progression of involves inactivation caused by mdm2 overexpression, and that p21 transactivation in this setting is due to an alternative system rather than through a p53-dependent signaling mechanism.

35 p53 responds to different forms of cellular stress by targeting and activating genes involved in growth arrest and cell death. A target of p53-induce transcription is the p21/WAF1 gene, which encodes a cyclin-dependent kinase

inhibitor (1). In addition, levels of p53 are tightly regulated by mdm2, which binds to p53 repressing its activity and triggering its degradation. The MDM2 gene is itself under the transcriptional control of p53, creating an 5 autoregulatory feedback loop (2).

Alterations in the TP53 gene appear to be uncommon in prostate cancer, and their clinical significance has not been fully investigated. A recognized limitation of most studies 10 is that they are confined to the analysis of p53 alterations, without analyzing other critical components that regulate its functions. The MDM2 gene is amplified in a variety of tumors, and mdm2 overexpression without amplification appears to be a common mechanism of p53 inactivation in certain cancers 15 (3,4). Lack of data regarding the functional status of the p53 products encountered in the tumors analyzed represents another drawback. It has been reported that p21/WAF1 gene expression may serve as an indicator of p53 activity, since p21/WAF1 is under the transcriptional control of p53. 20 However, serum or individual growth factors, such epidermal growth factor (EGF), and fibroblast growth factor (FGF), were shown to induce p21 expression in p53-deficient cells (5,6). Thus, there are at least two separate pathways accounting for the induction of p21, one linked to DNA-damage 25 recognition, and the other produced by signaling mechanisms caused by certain cellular mitogens.

In the present study, we have analyzed the patterns of p53 expression and those of critical components of its pathway, 30 namely mdm2 and p21, in 86 patients with prostate cancer. The association between these markers and clinicopathological parameters of poor outcome, including time to PSA relapse and proliferative index, were also examined.



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EXPERIMENTAL DETAILS

Experimental Details for Second Series of Experiments

5 MATERIALS AND METHODS

Patients. A total number of 86 patients who underwent radical prostatectomy at Memorial Sloan-Kettering Cancer Center in the period between 1990 through 1991 were studied. Patient selection was based on the availability of both 10 adequate clinical follow up and representative archival pathological materials for immunohistochemical analysis. The median age at the time of surgery was 65 years (range 46-74). Their median follow up was 64.5 months (range 10-94 months). Formalin-fixed, paraffin embedded prostate tissues were obtained from our archival tumor bank. Representative hematoxylin-eosin stained sections were examined to evaluate the histopathological characteristics of each case.

Clinicopathological parameters examined include pre-treatment 20 PSA, pathologic stage and Gleason score, both determined based on the radical prostatectomy specimen. Time to PSA relapse was calculated from the day of surgery to the first detectable PSA. PSA relapse was defined as three consecutive rise in PSA at least one week apart. Only patients who had undetectable PSA level after surgery were included in this analysis.

Tumors were staged pT2 (n=51) and pT3 (n=35).. Twenty-nine patients were Gleason score <7, while 18 patients were 30 Gleason ≥7. In six cases, due to scarcity of tumor representation in the specimen, grade was considered to be not interpretable. Thirty-three patients (38.3%) received neoadjuvant hormone treatment preoperatively, and were defined as hormone-treated. These patients had non-evaluable 35 Gleason scores. Patients who did not receive neoadjuvant hormone treatment were defined as hormone-naïve.

Monoclonal Antibodies and Immunohistochemistry. The following well characterized mouse monoclonal antibodies and corresponding final working dilutions were used for the present study: anti-p53 monoclonal antibody PAB1801 (Ab-2 CalBiochem/Oncogene Science, 5 clone; Boston, MA: dilution); anti-mdm2 monoclonal antibody 2A10 (a gift from Dr. Arnold Levine, Rockefeller University, New York, N.Y.; 1:500 dilution); and an anti-p21 monoclonal antibody (Ab-1 clone; CalBiochem/Oncogene Science; 1:20 dilution). An 10 anti-Ki67 mouse monoclonal antibody (clone MIB1; Immunotech SA, France; 1:50 dilution) was used to assess proliferative MIgS-Kp1, a mouse monoclonal antibody of the same subclass as the primary antibodies listed above was used as negative control.

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An avidin-biotin immunoperoxidase method was utilized. Briefly, sections were subsequently immersed in boiling 0.01% citric acid (pH 6.0) for 15 minutes to enhance antigen retrieval and incubated with primary antibodies overnight at Biotinylated horse anti-mouse IgG antibodies were 20 4°C. applied for 1h (Vector Laboratories, Burlingame, CA; 1:500 dilution), followed by avidin-biotin peroxidase complexes for 30 minutes (Vector Laboratories; 1:25 dilution). Diaminobenzidine was used as the final chromogen 25 hematoxylin was used as the nuclear counterstain. Nuclear immunoreactivity were classified on a continuous scale with values that ranged from undetectable levels or 0% to homogeneous staining or 100%.

30 Statistical Analysis. The three markers were analyzed both as percentage of tumor cells and as discrete variables based on a priori cut-points. The cut-point for p53 of >20% was based on our previous analysis of p53 alterations in bladder cancer that revealed a strong association between p53 point 35 mutation and p53 nuclear accumulation in >20% of tumor cells (7,8). For mdm2, the cut-point was based on what have been published correlating mdm2 overexpression in ≥20% of tumor





cells with worse clinicopathological parameters (9,10). The same principle applied to the Ki67 cut-point determination (11,12). For p21 the cut-point of >5% was based on our finding that normal prostate glands lack p21 expression, and 5 the observation of p21 nuclear staining and presence of mitotic figures indicating high proliferative activity of the tumors.

The association of percentage of tumor cells expressing the 10 markers with time to PSA relapse, while adjusting for other variables with known prognostic significance, was assessed using the Cox proportional hazards model (13). In addition, Kaplan-Meier estimation (14) was performed and the log rank test (15) employed to assess the univariate relationship 15 between the individual markers using cut points and time to PSA relapse.

The associations between Gleason group and the three biomarkers were assessed using Fisher's exact test (16). 20 Also, associations between the three markers and variables such as Ki67 proliferative index, stage, and hormone status were also assessed using the above test.

EXPERIMENTAL RESULTS

25

Experimental Results for the Second Series of Experiments

Table 1 summarizes the data in relation clinicopathological parameters, including pre-treatment PSA, 30 tumor stage, Gleason tumor grade, hormone proliferative index, and immunophenotype profile. Figure 7 illustrates the univariate relationships of the three markers with time to PSA relapse with Kaplan-Meier curves estimated.

Table 1. Summary Of Data In Relation To Immunophenotype Profile

		P53		p21		-d- o	
	(#)	(%)	(#)	(%)	(#)	ndm-2 (%)	
<u>PSA</u>						(4)	
<4	0/18		_				
4-10	3/28	0	5/18	27	3/18	16	
>10	-	10	7/28	25	7/28	25	
	3/40	7.5	, 10	40	18/40		
p value		. 374	4	.382	20/40	45	
Chana						.060	
<u>Stage</u>							
T<3	3/51	5.8	14/51	27	11/51	_	
T=3	3/35	8.5	14/35	40		21	
p value		.631		.222	17/35	48	
				.222		.009	
Gleason S	COTE						
<7	0/29	0	7/29	24	- /-		
=7	2/18	11	10/18	22	7/29	24	
NE	4/33	2	10/33	30	9/18	50	
p value		.157	10,55		11/33	33	
				.074		.190	
Hormone St	atus						
Naive	2/53	3	18/53				
Treated	4/33	12	10/33	33	17/53	32	
p value		.139	10/33	30	11/33	33	
		. 133		.725		. 904	
Proliferat	<u>ion Index</u>	K167					
Low	5/75	6	20/75				
High	1/11	9	20//5 8/11	26	22/75	29	
value	·	.768	0/11	72	6/11	54	
•		. / 68		.002		. 096	

p53 nuclear overexpression of >20% was observed in 6 of 86 The distribution of p53% expression was primarily patients expressing less than 5% p53 (n=76). The other 10 patients had varying levels of p53% expression, indicating 5 a very low frequency of p53 alteration in this group of patients. There is no correlation between p53 positive phenotype and pretreatment PSA, tumor stage, tumor grade, hormone status, or high proliferative index. Also, there is no association between p53 overexpression and p21 or mdm2 10 overexpression. A significant association was observed between p53 status determined by the cut-point and time to PSA relapse. This association is illustrated in Figure 7. Using the log rank test to examine the overall differences between p53 negative phenotype and p53 positive phenotype 15 revealed a statistical significant difference P<0.01.



indicates an obvious PSA relapse time advantage for patients who do not overexpress p53. However, the magnitude of this difference may not be reliably estimated due to the small number of patients and events in the p53 positive phenotype 5 group.

mdm2 nuclear overexpression of ≥20% tumor cells was observed in 28 of 86 cases (32.5%). mdm2 positive phenotype was associated with advanced stage (P=0.009). In addition, mdm2 overexpression was observed not to be significant with respect to a decreased time to PSA relapse (Figure 7). A trend was observed between mdm2 overexpression and higher pretreatment PSA (P=0.06).

15 p21 nuclear overexpression of >5% tumor cells was observed in 28 of 86 patients (32.5%). Patients with p21 positive phenotype were observed to have a significant association with high Ki67 proliferative index (P=0.002). High Ki67 porileferative index was identified in 11 of 86 patients 20 (12.7%). Patients with p21 positive phenotype had a significant association with decreased time to PSA relapse, as illustrated in Figure 7. Also, p21 overexpression was associated with mdm2 overexpression (P<0.01). However, no association was observed between identification of p21 and/or 25 mdm2 positive phenotype and p53 overexpression.

Forty-three of the total 86 patients had one or more altered markers. Patients with any alteration (p53 or mdm2 or p21) were observed to have a higher rate of PSA relapse (P< 0.01).

30

The multivariate relationship between the markers and time to PSA relapse was assessed using Cox proportional hazards model. It was of interest to examine the effect of the 35 markers while adjusting for variables with know prognostic significance. Both, p53 and p21 positive phenotypes were significant while adjusting for pre-treatment PSA and Gleason group (P<0.01 for both markers). Examination of the

overexpression of at least one marker (p53, mdm2 or p21) with respect to time to PSA relapse showed that this variable was also significant (P<0.01) while adjusted for pre-treatment PSA and Gleason group. Tumor stage (< 3 vs. ≥3) was not significant in either the univariate or multivariate analyses, and was thus excluded from the model. The model that seemed to account for the most information included p53 and p21, along with pre-treatment PSA.

10

EXPERIMENTAL DISCUSSION

Experimental Discussion for the Second Series of Experiments

15 Reports dealing with the frequency of TP53 mutations and p53 overexpression in prostate cancer have yielded conflicting results, alterations ranging from 2% to 65% of cases studied This discrepancy might be explained by relatively small number of cases and different disease stages 20 analyzed in some reports, the distinct methodologies employed, and the cutoff points used for evaluation of IHC However, a general finding was the association between p53 alterations and clinicopathological parameters of poor clinical outcome, such as high grade and late stage 25 (18,19,22). In this study, we observed a relatively low frequency of p53 nuclear overexpression in patients with localized prostate cancer, as previously reported (23,24). To determine the potential clinical relevance of identifying positive phenotype, we correlated phenotypic 30 characteristics of the tumors with the time to PSA relapse. This is considered the most sensitive indicator of success or failure following radical prostatectomy in patients treated for localized disease. Analysis of data revealed that p53 overexpression was significantly associated with PSA 35 relapse (P<0.01) and independent of pretreatment PSA and Gleason group. However, the magnitude of this difference may not be reliably estimated due to the small number of patients



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and events in the positive phenotype. We also observed that all patients who received neoadjuvant hormone treatment prior to surgery and had tumors that overexpressed p53 relapsed. This finding could be due to the advanced stage at which patients presented and were selected for treatment using this modality. Mechanistically, an altered p53 status in this setting could have conferred resistance to castration-induced apoptosis, ultimately leading to disease relapse. The association between p53 overexpression and hormone refractory prostate cancer has been reported in locally advanced and metastatic disease (25). However, to our knowledge, this is the first report to suggest that this association might be an early event in the evolution of hormone refractory disease in clinically localized prostate cancer.

15

In the present study we also analyzed alterations affecting other regulators of the p53 pathway in primary prostate cancer, including mdm2 and p21. The MDM2 gene maps to 12q13 and is found overexpressed in certain tumors, due to its 20 amplification as a component of an amplicon that includes other relevant genes, such as CDK4. The MDM2 is under transcriptional regulation by p53, and encodes a 90-kDa zinc finger protein (mdm2) which contains a p53-binding site (26). It has been shown that mdm2 binds to p53, and acts as a 25 negative regulator by inhibiting p53 transcriptional activity degradation, thus targeting its autoregulatory feedback loop (27). In this study, nuclear mdm2 overexpression was found in 32.5% of cases. We observed that mdm2 positive phenotype was significantly associated 30 with advanced stage. It has been previously reported that MDM2 is not amplified on primary prostate cancer, based on a study of 29 tumors analyzed by Southern blot hybridization The discrepancy between the rate of MDM2 gene amplification and protein overexpression has been described breast cancer (29,30). and Burkitt's lymphoma Furthermore, it was observed in soft tissue sarcomas that mdm2 overexpression, rather than its amplification, associated with worse clinical outcome (10). Based on data

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from this study, we can postulate that mdm2 overexpression is a frequent mechanism of p53 inactivation in prostate cancer, and in this context the MDM2 gene can be classified as an oncogene in this setting.

5

The p21/WAF1 gene encodes a nuclear protein member of the cyclin-dependent kinase inhibitory KIP family involved in senescence and cell quiescence (31). The p21/WAF1 gene is also transcriptionally regulated by p53. 10 induction could also be accomplished by a p53-independent pathway. Serum or individual growth factors, such as EGF and FGF, were shown to induce p21 in p53-deficient cells (32). Based on these data, it has been postulated that p21 induction could be activated through two separate pathways. 15 The rate of p21/WAF1 mutations in human cancer is very low However, there is an association between altered patterns of p21 expression and clinical outcome in certain tumors, such as bladder, colon, and heptocellular carcinomas Lack of p21 expression in these studies was 20 correlated with poor clinical outcome, an expected finding one postulates that p21 deficiency reflects inactivation. As a corollary to this hypothesis, the p21 negative phenotype observed in the above referred studies was usually associated with p53 alterations. However, in our 25 study we found that p21 positive phenotype was significantly associated with high proliferative index and overexpression, but not with p53 status. Moreover, patients with p21 positive phenotype had a significant association with decreased time to PSA relapse. p21 overexpression has 30 been reported to be associated with worse prognosis in other tumor types, including, breast, esophageal carcinoma, and squamous cell carcinomas of head and neck (37-39). Moreover, p21 overexpression was found to be associated with resistance to chemotherapy in acute myeloid leukemia and glioblastoma 35 (40,41).

These data could be interpreted as follows (see Figure 8). A positive p21 phenotype could signify activation of p53 in

response to DNA damage or cellular stress. This effect would result in G1 arrest of the prostate tumor cells expressing p21. We observed, on the contrary, an association between p21 positive phenotype and increased proliferative activity.

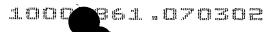
5 Thus, it is more plausible to postulate that the p21 overexpression observed is caused by a p53-independent transactivation mechanism. In the setting of prostate cancer, the alternative mechanism could be due to mitogenic stimuli via growth factor signaling. There is abundant 10 evidence regarding the upregulation of growth factor

receptor/ligand activity in prostate tumors (42-46). An additional aberration causing p53 inactivation would be required in this model to explain the lack of cell death and association with proliferative activity. It is our

15 hypothesis that the increased mdm2 expression discussed above provides this requirement, further supporting the oncogenic role of mdm2 in prostate cancer.

Finally, the association between p21 and high proliferative 20 index might also reflect deregulated cyclinD1/CDK4 activity. In fact, we observed a strong association between p21 positive phenotype and cyclin D1 overexpression in this cohort of patients (Drobnjak et al, personal communication). Taken together, these data supports the concept that p21 overexpression denotes an inefficient pRB control on S-phase entry.

Growth control in mammalian cells is accomplished largely by the action of the RB protein, regulating exit from the G1 30 phase, and the p53 protein, triggering growth arrest or apoptotic processes. In this group of patients, there is enough evidence to suggest that both mechanisms are defective in prostate cancer. The high proliferative index reflects the inefficient pRB control. We postulate that this phenomenon is produced by deregulated cyclinD1/CDK4 activity, which is associated with a p21 positive phenotype. The deactivation of a p53-dependent apoptosis could be explained by the degradation of p53 induced by mdm2 overexpression.



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In sum, alterations affecting the p53 pathway are frequent events in prostate cancer. It is our hypothesis that a pathway of prostate cancer progression involves p53 inactivation caused by mdm2 overexpression, and that p21 transactivation in this setting is due to an alternative signaling system rather than through a p53-dependent mechanism.

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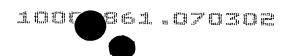
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THIRD SERIES OF EXPERIMENTS

Cyclin D1 is a key regulator of the G1 phase progression of the cell division cycle. There is an increasing evidence 5 that deregulated cyclin D1 expression is implicated in tumorigenesis and tumor progression in certain neoplasms. The present study was conducted in order to analyze the alterations affecting cyclin D1 in prostate cancer, as well as to assess its potential clinical significance. We studied 10 116 cases of primary (n=86) and metastatic (n=30) prostate and using immunohistochemistry carcinomas characterized monoclonal antibody to cyclin D1. were correlated with proliferative index, as assessed by Ki67 antigen expression and with clinicopathologic variables of 15 poor prognosis. Cyclin D1 positive phenotype, defined as identification of immunoreactivity in the nuclei of ≥20% tumor cells, was found in 26 of 116 (22%) significant association was observed between cyclin positive phenotype and clinicopathologic parameters, such as (P=0.045), evidence of bone 20 advanced tumor stage (T≥3) metastases (P=0.001) and with elevated preoperative prostate specific antigen measurements (PSA >10 ng/ml) (P=0.01). Ki67 proliferative index was considered high when ≥20% tumor cells displayed positive nuclear staining, a phenotype that was 25 observed in 20 of 107 (19%) evaluable cases. Moreover, high Ki67 proliferative index was associated with cyclin D1 overexpression (P=0.01). These data support the hypothesis that alterations of cyclin D1 may represent an oncogenic event in human prostate cancer. Furthermore, it appears that 30 cyclin D1 overexpression contributes to tumor progression in a subset of particularly aggressive prostate carcinomas, especially those developing osseous metastases.

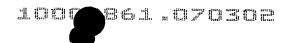
Prostate cancer has been reported to be a neoplastic disease 35 of a slow growth rate. Nevertheless, it still represents the second leading cause of cancer deaths in men in the United States. There is an obvious discrepancy between the clinical impression of a slowly growing neoplasm and tendency to



produce an aggressive metastatic disease in individual patients. The prognostic indicators of histologic grade, pathologic stage, DNA ploidy, and tumor cell proliferative index proved to be of limited value in determining the biologic behavior of prostate cancer (1-3). Tumor suppressor genes, particularly p53 and RB, implicated in the molecular genetics of many human malignancies, were reported to be

altered in a rather low frequency in prostate cancer (4-8).

10 Cell cycle transitions are controlled by functional heterodimers composed of a cyclin, acting as a regulatory subunit, and cyclin-dependent kinase (Cdk), which acts as the catalytic component (9). Multiple cyclins have been isolated and characterized, and a temporal map of their expression has 15 been delineated. It is postulated that the complexes formed by cyclin D1 and Cdk4 govern G1 progression, while cyclin E-Cdk2 controls entry into S-phase and cyclin A-Cdk2 affects the regulation through S-phase (10). Cyclin D1-Cdk4 complexes exert their function through the phosphorylation 20 of the product encoded by the retinoblastoma gene, pRb, in order overcome the cell cycle block imposed hypophosphorylated pRb (10). Several studies suggest that gene amplification and overexpression of cyclin D1 and Cdk4 are oncogenic events in certain tumors, including breast 25 cancer (11), head and neck tumors (12, 13), esophageal (14, 15) and colorectal carcinoma (16). We undertook this study in order to analyze patterns of cyclin D1 expression in prostate cancer. The alterations identified were correlated Ki67 proliferative index, as well as relevant 30 clinicopathologic parameters, in an attempt to define their potential biologic significance in prostate cancer.



EXPERIMENTAL DETAILS

Experimental Details for Third Series of Experiments

MATERIALS AND METHODS

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Patients Characteristics and Tissues. A cohort of 116 patients with prostate carcinoma were evaluated, consisting of 86 primary and 30 metastatic cases (eight metastases to lymph node and 22 metastases to bone). All primary tumors represented consecutive cases of patients underwent radical prostatectomy at Memorial Sloan-Kettering Cancer Center, in the period of 1990 and 1991. metastatic cases (n=30) were selected on the basis of the availability of tissue in the tumor bank. Samples were 15 formalin-fixed, paraffin embedded tissue specimens, obtained from the Department of Pathology at Memorial Sloan-Kettering Representative hematoxylin-eosin stained Cancer Center. sections of each paraffin block were examined microscopically to confirm the presence of tumor, as well as to evaluate the 20 pathologic grade and stage of the tumors analyzed. Thirtythree of 86 patients with primary carcinoma received preoperatively neoadjuvant hormone therapy (hormone treated), while the remaining 53 patients were not treated with such protocols and were considered hormone-naive. Hormone-naive 25 primary tumors with sufficient tumor representation on tissue sections were assigned histologic grade (n=47). Histologic grade was categorized into two groups: low grade (Gleason score <7), and high grade (Gleason score ≥7). According to pathologic stage, cases were grouped into early (organ 30 confined tumors, T_2), or advanced tumors (extending beyond The response variable time to prostatic capsule, $\geq T_3$). prostate-specific antigen (PSA) relapse was defined as the time from radical prostatectomy to the time of the first detectable (non zero) PSA measurement. Three consecutive 35 increases of PSA were required to confirm PSA relapse. nonmeasurable PSA after radical had a patients who prostatectomy were included in the analysis.

Monoclonal Antibodies and Immunohistochemistry. The following well characterized antibodies and corresponding final working concentrations were used for the present study: anti-cyclin D1 mouse monoclonal antibody (Ab-3, clone DCS-6, 5 IgG1, Oncogene, Calbiochem, Cambridge, MA; 1μ g/ml); anti-Ki67 mouse monoclonal antibody (clone MIB-1, IgG1, Immunotech, Marseille, France; $4\mu g/ml$). A nonspecific mouse IgG1 kappa monoclonal antibody was used as a negative control at similar working concentrations. Immunohistochemistry was performed 10 on $5\mu\mathrm{m}$ tissue sections using avidin-biotin-peroxidase method and antigen retrieval. Briefly, sections were immersed in boiling 0.01 M citric acid (pH 6.0) and heated in microwave oven for 15 minutes, to enhance epitope exposure. cooling to room temperature, slides were incubated with 10% 15 normal horse serum for 30 minutes. Subsequently, appropriately diluted primary antibodies were applied for overnight incubation at 4°C. Biotinylated horse anti-mouse IgG antibodies were used as secondary reagents, applied for an incubation period of 30 minutes (Vector Laboratories, 20 Burlingame, CA; 1:500 dilution), followed by avidin-biotinperoxidase complexes incubated for 30 minutes Laboratories - 1:25 dilution). Diaminobenzidine was used as chromogen and hematoxylin final as the nuclear counterstain.

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Immunohistochemistry Evaluation. Nuclear immunoreactivities for both cyclin D1 and Ki67 antigens, were classified into two categories defined as follows: negative (<20% tumor cells 30 displaying nuclear immunostaining), and positive (\geq 20% tumor cells with nuclear immunostaining). The appropriateness of this cutoff was validated graphically by using point predicted survival time and looking at specific immunoreactivities as a continuum data in this group of Ultimately, results were interpreted as defined 35 patients. above.

Statistical Methods. The baseline variables examined were (ng/ml) at time of diagnosis (divided into three categories: <4, 4-10 and >10), Tumor grade (Gleason score) (divided into two mutually exclusive categories: <7 or ≥7), 5 Pathologic stage T (2 or ≥3), and percent cyclin D1 and Ki67 expression. Statistical analyses were conducted to assess: 1) the correlation between immunophenotypic variables and clinicopathologic parameters such as: presentation status, tumor grade, pathologic stage, preoperative PSA, and hormonal 10 status; 2) the correlation among immunophenotypic variables; 3) association between immunophenotypes and PSA relapse free The Mantel-Haenszel chi-square test was used to assess the associations among the different variables and results were considered significant if the P value was <0.05. 15 The FREQ procedure in SAS was used for this study (17). associations between time to PSA relapse immunophenotypes were evaluated using the Log Rank test and Kaplan Meier estimates (18).

20 EXPERIMENTAL RESULTS

Experimental Results for the Third Series of Experiments

Table 2 summarizes immunohistochemical data in relation to clinicopathologic parameters. Figure 9 illustrates the 25 immunohistochemical staining patterns of cyclin D1 in representative cases of primary tumors and bone metastases.



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Table 2. Clinicopathologic parameters in Relation to Cyclin Dl Immunoreactivity

Table 2. C	linicopatholo	gic Para	meters	III Kela	cion to	Cyclin	DI IMMUI	oreactivity
Parameter	cyclin N	D1-(<20 (%)	%)	cyclin N	D1+(≥20 (&)	0%)	Total	P-value
Total Patients 9	0 (77.6)	26	(22.4)	116				
Presentation								
Primary tms	76	(88.4)		(11.6)	86			
LN metastases	7 (87.5)	1	(12.5)	8	NS			
Primary tms	76	(88.4)		(11.6)				
Bone metastases	7	(31.8)	15	(68.2)	22	0.001		
Ki67 proliferativ	ve							
Low (<20%)	71	(81.6)	16	(18.4)	87			
High (≥20%)	11	(55.0)	9	(45.0)	20	0.01		
Primary tumors 76	(88.4)	10	(11.6)	86				
rm. Grade (Gleaso	on) *							
Low (<7)	27	(93.1)	2	(6.9)		29		
High (≥7)	17	(94.4)	1	(5.6)		18	NS	
Path. Stage								
Early (T2) 48	(94.1)		(5.9)		51			
Advanced (≥T ₃)	28	(80.0)	7	(20.0)	35	0.045		
Hormonal status								
H. naive	49	(92.5)	4	(7.5)		53		
H. treated	27	(81.8)	6	(18.2)	33	NS		
Pretreatment PSA								
<4 ng/ml	17	(94.4)	1	(5.6)		18		
4-10 ng/ml	28	(100.0)		0	(0.0)		28	
	31	(77.5)	9	(22.5)	40	0.01		

^{*}Patients who had received neoadjuvant hormonal therapy (n=33) and tissue sections with inadequate tumor representation (n=6) were not assigned Gleason grade and were excluded from this analysis.

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Cyclin D1 was expressed in ≥20% tumor cells in 26 of 116 (22%) evaluable cases, corresponding to 10 of 86 (12%) primary lesions and 16 of 30 (53%) metastases. statistically significant association between cyclin D1 5 overexpression and the presence of bone metastases. observed that 15 of 22 (68%) bone metastases overexpressed cyclin D1, while only 10 of 86 (12%) primary tumors presented with this positive phenotype (p=0.001). Cyclin D1 overexpression was also associated with advanced 10 pathologic stage in primary tumors. We found that 7 of 35 advanced stage (extending beyond the tumors of displayed cyclin D1 capsule, $\geq T_3$) overexpression, compared to only 3 of 51 (6%) organ confined Cyclin D1 was also detected at tumors (T_2) (P=0.045). 15 increased percentage of tumor cells in patients with high initial pretreatment PSA values. Nine of 68 (13%) patients with PSA ≥10ng/ml were cyclin D1 positive compared to only 1 of 18 (5%) patients with PSA <4ng/ml (P=0.01). There was no association between cyclin D1 overexpression and tumor 20 grade (Gleason score) or hormonal status (hormone naive vs. In order to assess disease progression we hormone treated). after PSA failure time to evaluated the There was no association between cyclin D1 prostatectomy. nuclear overexpression and early relapse as defined by 25 increased PSA measurements after radical prostatectomy in these group of patients (p=0.2).

Cyclin D1 overexpression correlated well with high Ki67 proliferative index, which was scored as being high in 20 of 107 (19%) evaluable tumors. Nine of 20 (45%) tumors displaying high Ki67 proliferative index also possessed cyclin D1 nuclear overexpression, while only 16 of 87 (18%) cases with low Ki67 proliferative index overexpressed cyclin D1 (P=0.01). Nevertheless, Ki67 proliferative index alone was not associated with clinicopathologic parameters of poor outcome in this cohort of patients.



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EXPERIMENTAL DISCUSSION

Experimental Discussion for the Third Series of Experiments

5 Autopsy records show that by the age of 80, approximately 60-70% of men around the world, have histologic evidence of prostatic carcinoma (19). Although this fact indicates generally slow growing nature of this malignancy, there are vast differences in the progression rate and development of 10 clinically evident or metastatic disease in these patients during their lifetime. Prostate cancer progression tends to follow periprostatic and perivascular penetration, invasion along perineural spaces, pelvic lymph node metastases and particularly bone metastases (20). Almost one fourth of 15 newly diagnosed cases presents with lymph node and/or osseous metastases and only one fourth of those survive five years (21). We were interested in analyzing the molecular events that might be responsible for the progression of prostate cancer from indolent to a life threatening, metastatic 20 disease.

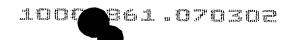
earlier reports on determining prostate proliferation, measured by flow cytometric S-phase fraction showed a positive predictive value of this variable and 25 prostate cancer progression (2). Tumors that demonstrate a higher proliferation rate are more likely to grow to and beyond prostatic capsule and to produce distant metastases. Recently, the cell division cycle regulatory mechanisms and their oncogenic role have become a major focus of cancer There is ever growing literature on cyclins and their associated kinases and their role in tumorigenesis Particularly D-family cyclins were implicated in specific human tumors. Bartkova et al. (23) report on a large group of various human malignancies, 35 carcinoma of the breast, uterus, colon, melanomas and soft sarcomas, high proportion of which tissue immunoreactivity for cyclin D1. By far the most frequent chromosomal abnormality that affects cyclin D1 in majority

of tumors is DNA amplification that results in increased expression of the RNA transcripts and protein levels (24). In some tumor types, however, immunohistochemistry proved to be the most accurate technique in determining deregulated 5 expression of cyclin D1 (11, 23). In this study we used immunohistochemistry to determine cyclin D1 expression in patients with prostate carcinoma. To our knowledge this first expression study on cyclin D1 in both primary tumors and bone metastases specimens. Only recently Kallakury et 10 al (25) evaluated the expression of $p34^{cdc2}$ and cyclin D1 in patients with radical prostatectomy. Results were correlated with conventional markers of poor prognosis. The authors showed no association between cyclin D1 immunoreactivity and clinicopathologic parameters, such as tumor grade, pathologic 15 stage, lymph node metastases and with disease free survival. Our data in this study, on the other hand, suggest the involvement of cyclin D1 in the progression of human prostate cancer. There was a remarkably significant difference in the levels of cyclin D1 expression between bone metastases and 20 primary tumors. There was an association between cyclin D1 immunoreactivity and tumors with advanced pathologic stage. correlated well with hiqh further Taken together, these results support proliferative index. the theory that increased levels of cyclin D1 expression 25 contribute to cell cycle imbalance with extremely shortened G1 phase and possibly with reduced cell requirements for growth factors to proliferate (26, 27). Subclones of tumor cyclins expression elevated with

In this study we conclude that cyclin D1 may play an oncogenic role in prostate cancer. Our data indicate that cyclin D1 is involved in tumor progression, particularly in a development of bone metastases. However, in order to determine the timeframe and prognostic value of this marker in prostate cancer, from the early onset to the evolution of metastatic disease, we intend to evaluate cyclin D1

uncontrolled growth advantage and contribute to tumor

30 progression.



immunophenotypes in paired samples of primary tumors and metastatic sites from the same patients.

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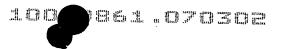
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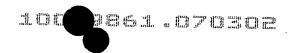
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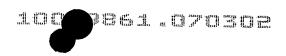


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FOURTH SERIES OF EXPERIMENTS

The INK4A gene maps to the region 9p21, and was initially described as encoding a 148 amino acid protein termed p16.

5 The p16 protein associates exclusively with Cdk4 and Cdk6, inhibiting their complexation with D-type cyclins, and the consequent phosphorylation of pRB. This contributes to cell cycle arrest. The purpose of the present study was to evaluate patterns of p16 expression in a well characterized cohort of prostatic adenocarcinomas, while exploring potential associations between alterations of p16 and clinicopathological variables.

Normal and malignant tissues from 88 patients with prostate situ hybridization examined. In 15 carcinoma were immunohistochemistry assays were used to determine the status of the INK4A exon 1α transcripts and levels of p16 protein, Associations between altered patterns of respectively. expression and clinicopathological variables, including 20 pre-treatment prostate-specific antigen (PSA) level, Gleason grade, pathologic stage, and hormonal status, were evaluated using the Mantel-Haenszel chi-square test. Biochemical (PSA) relapse after surgery was evaluated using the Kaplan-Meier method and the Log rank test.

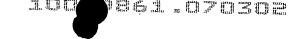
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The levels of p16 expression and INK4A exon 1α transcripts in normal prostate and benign hyperplastic tissues were However, p16 nuclear overexpression was undetectable. observed in 38 (43%) prostate carcinomas, while the remaining undetectable p16 showed cases (57%) 30 50 Overexpression of p16 protein was found to correlate with increased INK4A exon 1α transcripts. Moreover, p16 overexpression was associated with a higher pre-treatment PSA level (P=.018), the use of neoadjuvant androgen ablation 35 (P=.001), and a sooner time to PSA relapse after radical suggest that prostatectomy (P=.002). data These overexpression is associated with tumor recurrence and a poor clinical course in patients with prostate cancer.



The INK4A gene maps to the short arm of chromosome 9 (9p21), and was initially described as encoding a protein of Mr 15,845, termed pl6. (1,2). The pl6 protein forms binary complexes exclusively with Cdk4 and Cdk6, inhibiting their 5 kinase activity and subsequent pRb phosphorylation during the G_1 phase of the cell cycle. (1,3). Additional complexity results from the presence of a second INK4A product termed pl9ARF. (4-6) The pl9ARF protein has recently been shown to interact with mdm2 and to block mdm2-induced p53 degradation 10 and transactivational silencing(7,8). The two products, pl6 and pl9ARF, share exons 2 and 3 of the INK4A gene, but have distinct promoters and exon 1 units, exon 1α (p16) and exon 1β (p19^{ARF}). The INK4A gene is mutated in a wide variety of tumor cell lines and certain primary tumors (2, 9-14). In 15 addition, methylation of the 5' CpG island of the exon 1α promoter region is a frequent mechanism of pl6 inactivation in primary tumors (15, 16).

In prostate cancer the role of INK4A has not been well 20 elucidated, though analyses utilizing microsatellite markers in the vicinity of the INK4A gene have revealed loss of heterozygosity in a subset of primary and metastatic prostate tumors (17). Unlike reports of other primary tumors, INK4A inactivation, either through deletions, mutations, or through 25 promoter methylation, appears to be an infrequent event in The present study utilizes prostate cancer (18-23). immunohistochemical and in situ hybridization assays to examine patterns of p16 expression in a well characterized cohort of prostate cancer patients treated with radical 30 retropubic prostatectomy. Associations between altered p16 phenotypes and clinicopathological variables were also studied to further define their potential implications in prostate cancer.



EXPERIMENTAL DETAILS

Experimental Details for Fourth Series of Experiments

5 MATERIALS AND METHODS

Patient Characteristics and Tissues. A cohort of patients adenocarcinoma undergoing prostatic with prostatectomy at the Memorial Sloan-Kettering Cancer Center 10 from 1990-1991 was retrospectively evaluated. A total of 88 patients had adequate clinical follow-up and available pathological materials. The median age at the time of 65 years (range 46 - 74 years). The median surgery was follow-up time was 64.5 months (range 10 - 94 months). paraffin-embedded prostate tissues were 15 Formalin-fixed, obtained from the Department of Pathology. Representative hematoxylin-eosin stained sections were examined to evaluate the histopathological characteristics of each tissue section.

20 Clinicopathologic parameters examined included pre-treatment PSA, pathologic stage (24) and Gleason grade (25), both determined based on the radical prostatectomy specimen. Hormonal status of the patients was also evaluated. portion of the cohort (34 patients - 39%) was treated with and were defined 25 neoadjuvant androgen ablation hormone-treated. Patients who did not receive neoadjuvant therapy were defined as hormone naive. Additionally, biochemical relapse was examined. Relapse was defined as an elevation in the serum PSA level in a patient who had 30 previously demonstrated an undetectable PSA level postonly patients who had prostatectomy. That is, undetectable PSA level after surgery were included in the cohort, as this indicated that the surgical resection was complete and the patient was free of disease. Patients who 35 had PSA relapse were classified as treatment failures with tumor recurrence.



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An avidin-biotin immunoperoxidase Immunohistochemistry. assay was performed on formalin-fixed, paraffin-embedded tissue sections. Deparaffinized sections were treated with 1% H_2O_2 in order to block endogenous peroxidase activity. 5 Sections were subsequently immersed in boiling 0.01% citric acid (pH 6.0) in a microwave oven for 15 minutes to enhance antigen retrieval, allowed to cool, and incubated with 10% normal horse serum (Organon Tecknika Corp, Westchester, PA), to block non-specific tissue immunoreactivities. A well 10 characterized antibody to p16 (Ab-1, Oncogene Research Products, Cambridge, MA; 2ug/ml final concentration) was then incubated overnight at 4°C. Biotinylated horse anti-mouse IgG antibodies (Vector Laboratories, Inc., Burlingame, CA; 1:25 final dilution) were utilized as the secondary reagents. 15 This was followed by avidin-biotin immunoperoxidase complexes for 30 minutes. Laboratories, Inc.) Vector Diaminobenzidine was used as the final chromogen and nuclear counterstain. used as the hematoxylin was Immunoreactivities, assessed in tissue sections from a single 20 representative block in each case, were classified as a continuum of data from undetectable levels or homogenous staining levels (100%). Data was independently obtained by two observers, with minor inter-observer variability which was resolved by review of the problem 25 cases. Tumors were grouped into two categories defined as Group A (≤5% nuclear immunoreactivity in tumor cells) and Group B (>5% nuclear immunoreactivity in tumor cells).

Primers specific for the exon 1α 30 In Situ Hybridization. the INK4A gene were utilized to create sequence of digoxigenin-labeled probes for in situ hybridization. Probes a PCR-Script recombinant into cloned (Stratagene, La Jolla, CA). Plasmid DNA (lug) was linearized 35 using BamHI and XhoI. Antisense and sense riboprobes were generated from in vitro transcription of the linearized DNA polymerases, respectively. ТЗ RNA and using **T7**



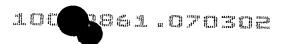
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Transcription was sustained for 2 hours at 37°C in 1X transcription buffer (Boehringer Mannheim, Indianapolis, IN), 20 U of RNAse inhibitor, 10 mmol/L each of ATP, GTP, CTP, 6.5 mmol/L UTP and 3.5 mmol/L digoxigenin-UTP. Deparaffinized 5 tissue sections were rinsed in water and PBS for 10 minutes. The slides were digested with Proteinase K (50 ug/ml) for 18 minutes at 37°C in PBS, and post-fixed at 4°C in a freshly prepared solution of 4% paraformaldehyde in PBS for 5 Prehybridization was done for 30 minutes at room and 2X 50% formamide 10 temperature (RT) in chloride/sodium citrate (SSC). The hybridization buffer consisted of 50% deionized formamide (v/v), sulphate (50% stock solution), 2XSSC (20X stock solution), 1% SDS (10% stock solution), and 0.25 mg/ml of herring sperm 15 DNA (10 mg/ml).

Hybridization was performed overnight at 45°C applying 10 50 of digoxigenin-labeled riboprobe in hybridization buffer per section under a coverslip. 20 coverslips were removed and the slides were washed in pre-warmed 2XSSC for 20 minutes at 42°C twice, followed by washes in pre-warmed 1XSSC and 0.5XSSC at 42°C for minutes. After these washes the slides were incubated in normal sheep serum diluted in buffer pH 7.5 and successively same buffer with anti-digoxigenin-AP the (Boehringer Mannheim) at a dilution of 1:500 for 1 hour at The visualization was accomplished by nitro-blue tetrazolium 5-bromo-4-chloro-3-indoylphosphate. The slides were counterstained with methyl green and mounted.

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INK4A exon-1α transcript levels were examined in a subgroup of 21 cases. Consecutive tissue sections were used to analyze p16 protein by immunohistochemistry and INK4A exon-1α transcript levels by in situ hybridization. As in the immunohistochemical analysis, tumors were grouped into two categories defined by the absence (≤5% tumor cells with cytoplasmic staining) or presence (>5% tumor cells with cytoplasmic staining) of transcripts.



Statistical Methods. The statistical analyses of the data from the 88 primary prostate cancer patients were conducted as follows. The response variable, time to PSA relapse, was defined as the time from radical prostatectomy to the time of first detectable PSA measurement. Patients who did not achieve a non-measurable PSA after radical prostatectomy were excluded from the analysis. Patients who were still alive at the time of analysis without relapse were censored at the date of last follow-up. The baseline variables examined were PSA measurement at time of diagnosis, hormone status, Gleason score (hormone naïve patients only), stage of disease, and percent p16 expression.

15 Associations between p16 expression and different categorical variables (hormone status, tumor grade, tumor stage, and pretreatment PSA levels) were assessed by Mantel-Haenszel chi-square test. Continuous variables, such as pre-treatment PSA, not known to follow a particular distribution were compared between two or more groups using Wilcoxon non-parametric tests.

The Cox proportional hazards model was used to examine the multivariate relationship between PSA relapse-free time from 25 prostatectomy and the baseline variables listed above. final model was determined using the "all subsets" procedure SAS PHREG and the Score criterion (26). As normal and benign tissues showed little to no pl6 expression, positive expression was described as >5% nuclear expression. 30 cutpoint was specified a priori and used for the subsequent Immunohistochemical and in situ statistical analysis. hybridization studies were completed, analyzed, and recorded blind to clinical information. Kaplan-Meier estimates of relapse-free survival stratified by pl6 classification were The LIFETEST procedure in SAS was used to 35 evaluated. generate the Kaplan-Meier estimates and the resulting survival curves (26, 27). The Log rank test was used to test the hypothesis of no survival differences between p16



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positive and p16 negative populations.

EXPERIMENTAL RESULTS

5 Experimental Results for the Fourth Series of Experiments

The normal human prostate displayed undetectable levels of p16 protein and INK4A exon 1α transcripts in ductal and acinar epithelial cells. A lack of p16 immunoreactivity in these cells was observed in hormone-treated and hormone naive cases. Fibromuscular stroma cells also showed undetectable exon 1α transcripts levels. A similar negative pattern of p16 expression was observed upon the examination of prostatic tissue affected with benign hyperplasia (Figure 10).

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potential clinical frequency and determine the To implications of p16 alterations in prostate cancer, we analyzed a cohort of 88 primary prostate carcinomas. patterns of pl6 protein expression were noted. We observed 20 that 50 of the 88 cases (57%) had very low (≤5% nuclear immunoreactivity; 7 cases) or undetectable (43 cases) levels of pl6 protein expression (Group A) (Figure 11A). subgroup of these cases we also performed in hybridization assays, which revealed that all cases had INK4A exon lα transcripts (Figure 11B). 25 undetectable However, we noted that 38 of the 88 cases (43%) displayed nuclear staining with anti-pl6 specific antibodies (Group B) (Figure 11C). Immunoreactivities in tumor cells were further stratified into three categories: 6% to 29% nuclear staining 30 (n=11 cases); 30% to 59% nuclear staining (n=15 cases); and 60% to 100% nuclear staining (n=12 cases). In a subset of these patients, we also conducted in situ hybridization assays with the INK4A exon 1α specific probe. All cases displaying positive immunoreactivities also displayed 35 moderate to high levels of exon 1α transcripts (Figure 11D).

Table 3 summarizes the associations between p16 phenotypes and clinicopathological variables, which were assessed by

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Chi-square analyses. Immunohistochemical detection of p16 was not associated with Gleason grade, described as either low (Gleason grade 4 - 6) or high (Gleason grade 7 - 10) (P=0.153). Similarly, no association was observed between 5 pl6 nuclear expression and pathologic stage, defined as organ-confined $(T_1,\ T_2)$ and non organ-confined $(T_3,\ T_4,\ or$ However, there was a strong lymph node+) (P=0.087). association between p16 nuclear expression and pre-treatment PSA levels, based on cutoff points of <4, 4-10, and >10 ng/ml 10 (P=0.018). A similar result was observed when PSA was assessed as a continuous variable (P=0.01). In addition, we noted a significant correlation between p16 expression and the use of neoadjuvant androgen ablation (P=0.001).

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Table 3 Association of pl6 Immunoreactivity with Tumor Grade,
Hormonal Status, Tumor Stage, and Preoperative PSA Levels

	P16 Immunoreac	tivity (& of p	oatients)	
	Number of			
	Subjects	≤5%	5%	p - value
All Subjects	88	50 (57%)	38(43%)	
Gleason Grade*	82			
< 7	30(37)	24 (80)	6 (20)	p=0.153
≥7	18(22)	11(61)	7 (39)	•
unable to evaluate	34 (41)			
Hormonal Status	88			
hormone naive	54 (61)	40(74)	14(26)	p=0.001
hormone-treated	34 (39)	10(29)	24(71)	-
Pathologic Stage	88	-		
T_2	53 (60)	34 (64)	19(36)	p=0.087
≥ T ₃	35 (40)	16 (46)	19(54)	_
Pretreatment				
PSA (ng/ml)	88			
<4.0	18(20)	14 (78)	4 (22)	
4-10	29(33)	19 (66)	10(34)	p=0.018
>10	41 (47)	17 (41)	24 (59)	•

^{*} Grading is based on the radical prostatectomy specimen. Patients who had received neoadjuvant androgen therapy were unable to be graded consistently. Six patients did not have Gleason grade information and were excluded from this analysis.

A strong association was also found between pl6 nuclear overexpression and tumor recurrence, defined as by biochemical (PSA) relapse. Increasing pl6 expression correlated with an increased relative hazard of relapse. 5 suggesting a continuous relationship of the data. Overall, tumor recurrence was observed in 34 of 88 cases (39%). Thirteen of 50 cases (26%) with undetectable-to-low p16 expression (Group A) developed tumor recurrence. tumor recurrence was observed in 21 of 38 cases (55%) with 10 pl6 nuclear overexpression (Group B) (P=0.002) (Figure 12). Nevertheless, in a multivariate analysis adjusted for tumor grade, pre-treatment PSA, and pathologic did not contribute prognostic overexpression of pl6 information over pre-treatment PSA, the strongest independent 15 predictor of tumor recurrence.



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Experimental Discussion for the Fourth Series of Experiments

Normal prostate tissues display undetectable levels of p16 protein and INK4A exon 1α transcripts. It has been reported 5 that p16 expression is low to undetectable in most normal human tissues analyzed (15, 28, 29). In support of these observations, there are relatively low and near-constant levels of p16 protein and mRNA throughout the cell cycle of normal lymphocytes in culture (30). The lack of p16 expression in hyperplastic glands parallels that of normal prostatic tissue. Based on these data, it is our hypothesis that these negative p16 phenotypes reflect basal physiologic levels of p16.

15 Primary prostatic adenocarcinomas revealed two distinct pl6 phenotypes. Most tumors were found to have undetectable or very low levels of pl6 protein expression (Group A - 57% of This was associated with low levels or absence of INK4A exon 1α transcripts. Another group of tumors showed 20 elevated pl6 protein expression (Group B - 43%) which was consistently associated with increased INK4A These findings suggest an upregulation of the transcripts. $INK4A-\alpha$ gene, resulting in p16 protein overexpression. more aggressive course, had a in Group В Patients 25 demonstrated by high levels of pre-treatment PSA (P=.018) and a sooner time to biochemical (PSA) relapse (P=.002). A worse prognosis for Group B is also revealed by the trending association of pl6 overexpression with higher pathologic stage.

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The negative phenotype observed in Group A might correspond to the normal physiologic state, reflecting low-to-undetectable pl6 levels. Alternatively, it could be related to mutations affecting the INK4A gene, especially homozygous deletions, or methylation of the INK4A exon 1α promoter region. Nevertheless, it has been reported that these events are infrequent in prostate cancer (17-23). Furthermore, it appears the tumors with INK4A mutations have a more



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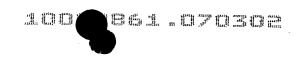
aggressive clinical course (31-33). Contrary to this, in the present study, we observed that Group A patients had a less aggressive behavior than Group B patients. For these reasons, we hypothesize that the negative phenotype observed in Group A is more likely a reflection of the normal physiologic state.

The up-regulation of the INK4A- α gene, resulting in the overexpression of p16 protein, may develop through different 10 mechanisms. An association between increased pl6 transcript and protein levels occur in tumor cell lines and certain primary neoplasms that lack functional pRb (1, Moreover, p16-mediated inhibition of cell cycle progression appears to be dependent upon functional pRb (38, 39). 15 data support an association between p16 and pRb, absence of functional pRb limits p16 activity and possibly promotes INK4A-α upregulation. Alternatively, enhanced activation of the $INK4A-\alpha$ gene may occur. E2F1, a direct activator of the INK4A exon 1\$\beta\$ promoter, does not appear to 20 directly activate INK4A- α transcription (40). evidence does exist for an indirect effect, overexpression has been reported to markedly increase p16 and p16-related CKI activity transcripts Overexpression of cyclin D1 and/or of Cdk4 may also influence 25 pl6 expression, through a compensatory feedback loop where deregulation of cyclin D/Cdk4 complexes results in increased levels of p16 protein (28, 42). In summary, it appears that an altered RB axis could trigger p16 overexpression in certain systems.

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Cellular stress produced by replicative senescence (43-45), hyperthermia (46), and UV irradiation (47) has been reported to trigger p16 overexpression. In the present study, another type of cellular stress, androgen ablation, may account in part for this observed phenomenon. A subset of patients were treated with neoadjuvant androgen ablation, a strategy reported to decrease the incidence of positive surgical margins after prostatectomy (48). In the present study, p16





overexpression was observed in 71% of hormone-treated versus 26% of hormone-naive patients (P=.001). These data suggest that p16 expression may be enhanced by androgen depletion. Androgens are known to modulate the expression of other CKI's such as p27 and p21 (49). In addition, it has been reported that the presence of androgens triggers downregulation of p16 in INCaP cells (50), a finding consistent with our observation of p16 overexpression in cases of androgen ablation. It is also possible that the association between p16 expression and androgen ablation may, in part, reflect staging bias by clinicians. In this setting, patients thought to have advanced disease may have been treated with neoadjuvant therapy.

- 15 Based on the the above referred data, it is our working hypothesis that pl6 overexpression in prostate cancer represents an altered phenotype, which identifies a subgroup of patients with a higher likelihood of post surgical failure and tumor recurrence. In support of this postulate, a preliminary report in prostate cancer has demonstrated an association between pl6 overexpression and poor outcome, as related to biochemical failure (51). In addition, pl6 overexpression has been associated with tumor progression and a poor prognosis in ovarian (52) and breast cancers (37).

 25 Though pl6 acts as a negative cell cycle regulator, specific mechanisms may contribute to its altered expression,
- mechanisms may contribute to its altered expression, overcoming pl6-mediated tumor suppressor activities. Ongoing studies may elucidate mechanisms of pl6 overexpression relative to androgen depletion and/or alterations in the RB 30 axis.



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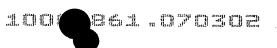
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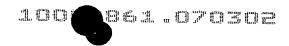
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FIFTH SERIES OF EXPERIMENTS

ABSTRACT

of HER-2/neu gene and Amplification Background: overexpression of its encoded product, the p185neu (HERtyrosine kinase membrane receptor, 5 2/neu) associated with tumor progression in certain neoplasms. Purpose: We conducted this study in order to investigate patterns of HER-2/neu protein expression in prostate cancer, analyzing different points in the natural and treated history of the disease. Methods: Eighty-three radical prostatectomy 10 cases and 20 metastatic lesions were studied for the association between HER-2/neu protein overexpression detected by immunohistochemistry and clinicopathological parameters including time to PSA relapse. Results: HER-2/neu protein overexpression, defined as complete membrane staining in >10% 15 of tumor cells using the FDA-approved DAKO kit, was found in 9 of 45 (20%) of evaluable hormone naïve primary tumors and 23 of 34 (67%) primary tumors after androgen deprivation therapy (P=0.0001). Of the 20 metastatic lesions, positivity was noted in 16 (80%) of the cases. On univariate analysis, 20 HER-2/neu overexpression was associated with pretreatment PSA relapse (P=0.02). and time to PSA controlling for pretreatment PSA, the association between HER-2/neu treatment was still and (P=0.0003). No association was found between HER-2/neu 25 overexpression and Gleason score, capsular invasion, and tumor proliferative index determined by Ki67. Conclusions: These data suggest that there is significant HER-2/neu overexpression in primary tumors that persist after androgenalso emphasizes the importance of Ιt deprivation. 30 characterizing tumors at determined points in the natural or treated history of prostate cancer when targeting treatment to specific biologic processes.



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INTRODUCTION

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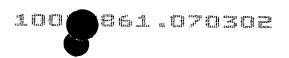
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HER-2/neu protein is a transmembrane tyrosine kinase receptor with high homology to the epidermal growth factor receptor (1). Amplification of the HER-2/neu gene and overexpression of its encoded protein have been observed in certain tumor types, including breast, ovary, and lung carcinomas (2-4). In prostate cancer, several studies have reported HER-2/neu gene amplification or protein overexpression to variable degrees in cell lines (5), xenografts (6), as well as in primary tumor samples (7,8). Little consideration, in the literature, has been given to the point in the history of disease that the tumor sample being analyzed represents. biopsies between diagnostic distinction prostatectomy specimens, the specifics of prior therapy administered, and whether the tumor was obtained from the prostate or metastatic lesion are not reported consistently in different series. Disparate levels of reported HER-2/neu expression in prostate cancer may also be due to the lack of standardization of the immunohistochemical assays used, the antibody used to assess HER2 status, distinct antigen recovery strategies, and scoring methodologies with different definitions of "abnormal" (9-13).

The current study focused on the pattern of HER-2/neu protein expression in prostate cancers representing two distinct 25 standardized with assessed states clinical immunohistochemical assay (14): localized disease (pre- and post-androgen ablation), and androgen-independent metastatic The associations between patterns of HER-2/neu tumors. clinicopathological standard expression and 30 protein parameters of poor outcome were also examined.



MATERIALS AND METHODS

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Clinical and Pathological Data.

A cohort of 103 patients with prostate cancer was studied, including 83 cases with localized tumors and 20 different patients with metastatic lesions. The 83 localized tumors were obtained for the study by radical prostatectomy performed between 1990 and 1991 at Memorial Sloan-Kettering Cancer Center, and patients were followed up at the center. Twenty metastatic lesions from patients with progressive androgen-independent disease were also analyzed. were formalin-fixed paraffin-embedded tissue specimens. Representative hematoxylin-eosin stained sections of each paraffin block were examined microscopically to confirm the presence of tumor, as well as to evaluate the pathological grade and stage of the primary tumors analyzed. Thirty-four of the 83 patients with clinically localized tumors received preoperative neoadjuvant androgen ablation therapy, while the remaining 49 patients were hormone-naïve. Forty-five of the hormone-naïve primary lesions with sufficient tumor tissue sections were assigned representation on histological grade. Cases were grouped as low Gleason score (<7, n=28), and high Gleason score (\geq 7, n=17). androgen deprivation samples were not graded (15). According to pathologic stage, cases were grouped into organ confined tumors (pT2, n=50), or tumors extending beyond prostatic capsule $(T \ge 3, n=33)$. The response variable time to prostate-specific antigen (PSA) relapse was defined as the time from radical prostatectomy to the time of the first detectable (non-zero) PSA. Three consecutive increases of PSA were required to confirm PSA relapse; however, the time of relapse was taken as the time of the first detectable PSA Patients who did not achieve a non-measurable PSA value. after radical prostatectomy were excluded from the analysis. The twenty metastatic androgen-independent cases were all bone lesions.



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Immunohistochemical Analysis of HER-2/neu Expression. The Herceptest Immunohistochemical kit (DAKO Carpenteria, CA) was used as previously described (16,17). Membrane immunoreactivities for HER-2/neu protein were categorized as undetectable or "zero" to +3 category, as defined by the developers of the commercial kit, and compared with the supplied positive and negative controls. "zero" is defined as undetectable staining or membrane staining in less than 10% of the tumor cells. Score +1 is defined as faint membrane staining detected in more than 10% Score +2 was considered as weak to of the tumor cells. moderate complete membrane staining observed in more than 10% Finally, score +3 was defined as a of the tumor cells. moderate to strong complete membrane staining observed in >10% of the tumor cells. HER-2/neu protein expression was classified into two categories defined as follows: negative (scores 0 and 1) and positive (scores 2 and 3), The cut off point was used based on reported studies in breast cancer (16,17) and as approved for use by the US Food and Drug Administration.

Immunohistochemical Analysis of Ki67 Expression. proliferative activity was assessed by the anti-Ki67 monoclonal antibody MIB1 (Immunotech Corp., France; 1:50 dilution). Clone MIgs-KpI, a mouse monolconal antibody of the same subclass as MIB1, was used as a negative control at similar working dilution (Pharmingen Laboratories, San Diego, CA). Sections were immersed in boiling 0.01% citric acid (pH 6.0) for 15 minutes to enhance antigen retrieval, allowed to cool, and incubated with the primary antibody overnight at Biotinylated horse anti-mouse IgG antibodies were applied for 1 hour (Vector Laboratories, Burlingame, CA; avidin-biotin peroxidase followed by dilution), (Vector Laboratories; minutes complexes for 30 dilution). Diaminobenzidine was used as the final chromogen, and hematoxylin as the nuclear counterstain. immunoreactivities were classified into two categories: negative (<20% of tumor cells displaying nuclear staining)

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and positive (\geq 20% tumor cells displaying nuclear staining). Ki67 proliferative index was considered high when \geq 20% of tumor cells displayed a positive MIB1 nuclear staining pattern (18,19).

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Fluorescence "In Situ" Hybridization (FISH). We conducted FISH analyses using a HER-2/neu gene copy number in 66 cases using a unique sequence HER-2/neu probe (Ventana Medical System, Tucson, AZ). The assay was considered to detect gene amplification if more than 4 copies of the HER-2/neu gene were identified in at least 40 tumor cells.

Statistical Analyses. The baseline variables examined were PSA (units) at time of diagnosis, Gleason score (divided into two mutually exclusive categories: <7 or ≥7), T stage of disease (pT2 or ≥ pT3), and HER-2/neu membrane expression patterns (negative or positive, see above). Statistical analyses were conducted to explore: 1) the association between immunophenotypic variables and clinico-pathologic parameters, such as tumor grade, tumor stage, preoperative PSA, and hormonal status; and 2) the association between HER-2/neu phenotypes and PSA relapse free survival. The Fisher's exact test was used to assess the associations among the different variables, and results were considered significant if the P value was <0.05 (20). The FREQ procedure in SAS was used for this study (21). The LOGISTIC procedure in SAS, using the Wald test, was used to assess the univariate association between preoperative PSA and HER-2/neu phenotypes considering PSA as a continuous variable (21). univariate associations between preoperative PSA and hormonal status was also explored, while the univariate associations between time to PSA relapse and HER2 immunophenotype was evaluated using the log rank test (22).distributions were generated using the Kaplan-Meier estimate The Cox proportional hazards model was employed to examine the relationship between time to PSA relapse and HERoverexpression after controlling for protein 2/neu



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pretreatment PSA and hormone treatment (24). A Wald test was used to test for an association between hormonal status and HER-2/neu overexpression controlling for pretreatment PSA (21).

RESULTS

Table 4 summarizes immunohistochemical data in relation to clinicopathological parameters. Figure 13 illustrates the immunohistochemical patterns of HER-2/neu protein expression in representative tumors with different staining scores compared to the control. In normal prostate samples, as well as in normal and benign hyperplastic glands, we observed HER-2/neu expression in basal cells, which served as internal controls for the evaluation of HER-2/neu immunostaining. In contrast, luminal (or secretory) cells in the normal glands were unreactive to HER-2/neu antibodies.

HER-2/neu membrane overexpression was observed in 32 of 83 (38.5%) of the radical prostatectomy cases (Table 4). Twenty-two (26.5%) cases were scored as zero, 29 (35%) cases were scored as +1, and 32 cases (38.5%) were considered +2 (Figure 13). This last value was used to define the cut-off point for HER-2/neu protein overexpression. We did not observe staining score of +3 as per the DAKO kit control in this cohort of patients.

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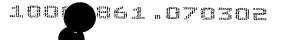
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Twenty-three of 34 (67%) patients who received neoadjuvant androgen ablation therapy were found to have HER-2/neu protein overexpression, versus 9 of 45 (20%) patients who were hormone naive at the time of radical prostatectomy. This association was statistically significant (P=0.0001). We also observed an association between baseline PSA and receipt of neoadjuvant hormones (P=0.0004). This association, coupled with the observed association between pretreatment PSA and HER-2/neu protein overexpression (P=0.011), suggests that pretreatment PSA may be a confounding factor in the hormone treatment and HER-2/neu between relationship expression. However, after controlling for pretreatment PSA the association between hormone treatment and HER-2/neu



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expression still exists (P=0.0003). We also found that 16 of the 20 (80%) androgen independent metastatic cases displayed HER-2/neu protein overexpression. Three cases (15%) were scored as zero, one case (5%) was scored as +1, ten cases (50%) were scored as +2, and six cases (30%) were considered +3.

association was observed between HER-2/neu protein (P=0.36), or Ki67 tumor stage overexpression and proliferative index (P=0.74). The same observation was seen analyzing hormone-naïve group, as no association was observed between HER-2/neu protein overexpression and tumor stage (P=0.265), Gleason score (P=0.071) or Ki67 (P=0.583). An HER-2/neu between protein association found was overexpression and time to PSA failure after radical prostatectomy (P=0.02), however, after adjusting for pretreatment PSA and hormone treatment, the association between HER-2/neu protein overexpression and time to PSA relapse was not significant (P=0.94).

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A significant number of FISH procedures were unsuccessful with failure to obtain control hybridization. Only two cases of 66 cases revealed HER-2/neu gene amplification. The two cases displaying HER-2/neu gene amplification also showed a HER-2/neu protein overexpression phenotype.

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TABLE 4

Clinicopatholo						
Parameter	HER-2 Negative		HER-		Total P-valu	
			Posi			
	#	8	#	8		
Total	51	61.5	32	38.5	83	
Path stage				2.4	F.0	
pT2	33	66	17	34	50	•
≥ pT3	18	55	15	45	33	0.
Pre-treatment	PSA					
<10	33	76	10	24	43	
≥10	18	45	22	55	40	0.0
Ki Index						
<20%	45	63	26	37	71	
≥20%	6	54	5	46	11	0.
Hormone Status				6 7	34	
Neoadjuvant	11	33	23	67		<0.0
Naive	36	80	9	20	45	<0.0
Relationship	of	Н	R-2/neu	Overe	pression	
Clinicopatholo	gical	Param	eters in	Hormone	Naive P	~~~+
CTIBICODACHOTO	9-0-					LUBL
Cancer (n=45).						<u>ros</u> t
Cancer (n=45). Gleason Score						<u>ros</u> c
<pre>Cancer (n=45). Gleason Score <7</pre>	23	82	5	18	28	
Cancer (n=45). Gleason Score						
<pre>Cancer (n=45). Gleason Score <7</pre>	23 14	82 14	5 3	18 23	28 17	
Cancer (n=45). Gleason Score <7 ≥7	23 14 24	82 14 86	5 3 4	18 23	28 17 28	0.0
Cancer (n=45). Gleason Score <7 ≥7 Path stage	23 14	82 14	5 3	18 23	28 17	0.0
Cancer (n=45). Gleason Score <7 ≥7 Path stage <t2 td="" ≥t3<=""><td>23 14 24 12</td><td>82 14 86</td><td>5 3 4</td><td>18 23</td><td>28 17 28</td><td>0.0</td></t2>	23 14 24 12	82 14 86	5 3 4	18 23	28 17 28	0.0
Cancer (n=45). Gleason Score <7 ≥7 Path stage <t2 pre-treatment<="" td="" ≥t3=""><td>23 14 24 12</td><td>82 14 86 71</td><td>5 3 4 5</td><td>18 23 14 29</td><td>28 17 28 17</td><td>0.0</td></t2>	23 14 24 12	82 14 86 71	5 3 4 5	18 23 14 29	28 17 28 17	0.0
Cancer (n=45). Gleason Score <7 ≥7 Path stage <t2 <10<="" pre-treatment="" td="" ≥t3=""><td>23 14 24 12 PSA 28</td><td>82 14 86 71</td><td>5 3 4 5</td><td>18 23 14 29</td><td>28 17 28 17</td><td>0.0</td></t2>	23 14 24 12 PSA 28	82 14 86 71	5 3 4 5	18 23 14 29	28 17 28 17	0.0
Cancer (n=45). Gleason Score <7 ≥7 Path stage <t2 pre-treatment<="" td="" ≥t3=""><td>23 14 24 12</td><td>82 14 86 71</td><td>5 3 4 5</td><td>18 23 14 29</td><td>28 17 28 17</td><td>0.0</td></t2>	23 14 24 12	82 14 86 71	5 3 4 5	18 23 14 29	28 17 28 17	0.0
Cancer (n=45). Gleason Score <7 ≥7 Path stage <t2 <10="" index<="" ki="" pre-treatment="" td="" ≥10="" ≥t3=""><td>23 14 24 12 PSA 28 8</td><td>82 14 86 71 90 57</td><td>5 3 4 5</td><td>18 23 14 29</td><td>28 17 28 17 31</td><td>0.0</td></t2>	23 14 24 12 PSA 28 8	82 14 86 71 90 57	5 3 4 5	18 23 14 29	28 17 28 17 31	0.0
Cancer (n=45). Gleason Score <7 ≥7 Path stage <t2 <10="" pre-treatment="" td="" ≥10<="" ≥t3=""><td>23 14 24 12 PSA 28</td><td>82 14 86 71</td><td>5 3 4 5</td><td>18 23 14 29</td><td>28 17 28 17</td><td>0.0</td></t2>	23 14 24 12 PSA 28	82 14 86 71	5 3 4 5	18 23 14 29	28 17 28 17	0.0

^{*} p-value generated from the Wald test using SAS procedure LOGISTIC where PSA is a continuous variable



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DISCUSSION

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This study shows the importance of evaluating tumors representing specific points in the natural history of prostate cancer (14). In untreated hormone-naïve primary tumors, HER-2/neu expression was infrequent (20%). In contrast, overexpression was observed in 80% of metastatic cases, and 67% of primary tumors surviving after androgen ablation. These patterns of HER-2/neu expression in prostate cancer should be regarded as "deregulated" rather than "ectopic," since HER-2/neu is detected in the basal cells of normal prostate glands.

Overall, HER-2/neu membrane overexpression was observed in 38% of the radical prostatectomy specimens. However, with reported rates of HER-2/neu overexpression in prostate cancer ranging from 0% to 94% it is difficult to determine a precise estimate (26-33). An evaluation of methodological differences between the situations helps to clarify the significance of These include the nature of the material the outcomes. studied, as well as the method of assessment. regard, we used a standardized kit and established cut-off values, albeit validated for breast cancer. We observed a correlation between score +2 overexpression and PSA relapse. This is the same cut-off value utilized in the context of breast cancer studies (16,17). We have also noted that HER-2/neu immunostaining in primary prostate cancer specimens is heterogeneous and focal. None of the primary tumors was scored as +3; however, 30% of metastatic lesions had a score In addition, we found that 80% (16 out of 20) of tumors representing androgen-independent metastatic disease overexpressed HER-2/neu protein. This shows the contribution of prior therapy and clinical state to overall outcomes.

HER-2/neu protein overexpression in primary tumors was compared to gene amplification using FISH in 66 cases. None of the HER-2/neu negative tumors showed amplification, while



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two of the HER-2 /neu positive cases revealed amplification signals. HER-2/neu overexpression in the absence of gene amplification may be due to transcriptional and post-translational mechanisms (36), a phenomenon that is also clinically frequent for other oncogenes such as cyclin D1 and mdm2 (37,38).

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A recent study on prostate cancer reported that 8 of 86 (9%) cases displayed HER-2/neu gene amplification; however, only one of these 8 tumors had a "moderate" amplification signal, while the remaining seven tumors were all described to have "low" amplification signals (39). It appears that, despite several earlier studies employing a FISH-based assay that found higher gene amplification rates (31,40), the frequency of HER-2/neu amplification in primary prostate carcinoma is generally lower than that reported in other tumor types, (3,41).including ovary and larynx cancer significant association was observed between HER-2/neu overexpression and prior androgen deprivation, a factor often considered as a prognostic factor. Even after controlling for the confounding effect of pretreatment PSA, this association was still observed.

while the mechanisms that contribute to the higher frequency of an altered HER2 status in tumors of different stages, suggests a role for HER-2/neu signalling in cell survival. This is supported by recent reports in which specific interactions between HER-2/neu and the androgen receptor have been described (42,43). Forced overexpression of HER-2/neu in androgen-dependent prostate cancer cells allowed ligand-independent growth. In this setting, HER-2/neu was able to activate the androgen receptor signaling even in the absence of the ligand, namely androgens. This "cross talk" is probably bi-directional, meaning that androgen ablation, known to down-regulate androgen receptors, could also upregulate HER-2/neu in response to cellular stress.

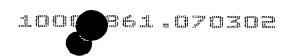


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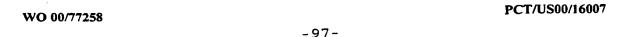
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An alternative explanation is that the higher frequency of positivity in neoadjuvant treated tumors is simply a function of disease extent. The association observed between HER-2/neu overexpression and higher pre-treatment PSA is consistent with this postulate. Similarly, the association between HER-2/neu2 overexpression and time to PSA relapse in this cohort may also reflect the more advanced nature of the tumor treated in this cohort. Against this is the fact that the association between HER2 status and prior hormone exposure persisted after controlling for baseline PSA.

The present study emphasizes the importance of characterizing the clinical state of the patient from which the tumor is studied. Based on our observation, we believe that detailed information regarding prior hormone exposure is essential when designing clinical trials targeting HER2 and other signaling molecules associated with prostate cancer progression. In that regard, xenograft studies with targeted therapy to HER-2/neu demonstrated disparate responses dependent on the androgen status of the prostate cancers (44).

ACKNOWLEDGEMENTS

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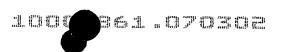
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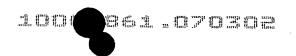
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Response of Prostate Cancer To Anti-Her-2/neu Antibody In Androgen-Dependent And Independent Human Xenograft Models.

Antibody to the Her-2/neu gene product has been shown to inhibit the growth of breast cancer cells overexpressing Her-2/neu and to have clinical utility in treating breast cancer. We studied a recombinant, humanized anti-Her-2/neu antibody (Herceptin) in preclinical models of human prostate cancer. The androgen-dependent CWR22 and LNCaP human prostate cancer xenograft models and androgen-independent sublines of CWR22 Her-2/neu staining of the parental, androgendependent, and androgen-independent CWR22 tumors and LNCaP tumors demonstrated variable Her-2/neu expression. Herceptin was administered i.p. at a dose of 20mg/kg twice weekly after No effect of Herceptin the xenograft had been established. on tumor growth was observed in any of the androgenindependent tumors; however, significant growth inhibition was observed in both of the androgen-dependent xenograft models, CWR22 (68% growth inhibition at the completion of the experiment; P=0.03 for trajectories of the average tumor volume of the groups) and LNCaP (89% growth inhibition; There was a significant increase in prostatespecific antigen (PSA) index (ng PSA/ml serum/mm3 tumor) in Herceptin-treated androgen-dependent groups compared with control (CWR22, 18-fold relative to pretreatment value versus 1.0-fold, P=0.0001; LNCaP, 2.35-fold relative to pretreatment value versus 0.6-fold, P=0.001). When paclitaxel (6.25mg/kg s.c., five times/week) was given to animals with androgendependent and independent tumors, there was growth inhibition 30 in each group. Paclitaxel and Herceptin cotreatment led to greater growth inhibition than was seen for the agents individually. Thus, in these prostate cancer model systems, Herceptin alone has clinical activity only in the androgendependent tumor and has at least an additive effect on 35 growth, in combination with paclitaxel, in both androgendependent and androgen-independent tumors. Response to



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Herceptin did not correlate with the PSA levels, because the PSA index markedly increased in the Herceptin-treated group, whereas it remained constant in the control group. These results suggest the utility of Herceptin in the treatment of human prostate cancer.